



human  
tez1  
EST2  
p123

Motif 0

AKFLHMLSVVVELLSFFVYVTTTFQKNR  
ISEIEWLVLGKRSNAKMCISDFEKRKQIFAEFIYWLNSFIPILOQFFYITESSDLNR  
LKDFRWLFISD---IWFTKHNFENINQLAICFISWLFRLIPKIIQTFYCYTEISSTVT-  
TREISWMQVET-SAKHFYYPDHEN-IYVLKLLRWIFEDLVVSLIRCFYVTEQQKSYSK  
\* . . . . . \*\*\* \*\*

human  
tez1  
EST2  
p123

Motif 1

LFFYRKSVMKLSQSIGIRQHILKRVQLRDVSEAEVRQHREARPAALLTSRLRFIPKP--DGL  
TVYFRKDIWKLRCRPI-TSMKWEAFKINENNVRMDTQK-TTLPFAVIRLLPKK--NTF  
IVYFRHDTWNLITPFIVEYFKTYLVENNVCNRHNSYTLS--NFNHSKMRIIPKKSNEF  
TYYYRKNIDVIMKMSI-ADLKKEITLAEVQEKEVEEWKKS-LGFAPGKIRLIPKK--TTF  
\* . . . . . \* . . . . . \* . . . . . \*

human  
tez1  
EST2  
p123

Motif 2

RPVNM DYVVGARTFRREKRAERLTSRVKALF-SVLNVERA  
RLITN-LRKRLIKVGSNKKMLVSTNQTLRPVASILKHLINEESSGIPFNLEVYMKLLTF  
RIIAIPCRGADEEFTIYKENHKNAIQPTQKILEYLRNKRPTSTKIYSPTQIADRIKEF  
RPIMTFNKIIVNSDRKTKITNTKLLNSHLMKTLKN-RMFKDPPGFAVFNYYDDVMKKY  
\* \* . . . . . \*

tez1  
EST2  
p123

Motif 3 (A)

KKDLLKHRMFGK-KKYFVRIDIKSCYDRIKQDLMFRIVKK-KLKDPEFVIRKYATIHATS  
KQRLKKFNNVLPELYFMKFDVKSCYDSIPRMECWRILKD-ALKNENGFFVRSQYFFNTN  
EEFVCKWKQVGPQLFFATMDIEKCYDSVNREKLSFTFLKTKLLSSDFWIMTAQILKRN  
\* \* . . . . . \* . . . . . \*

FIG. 1

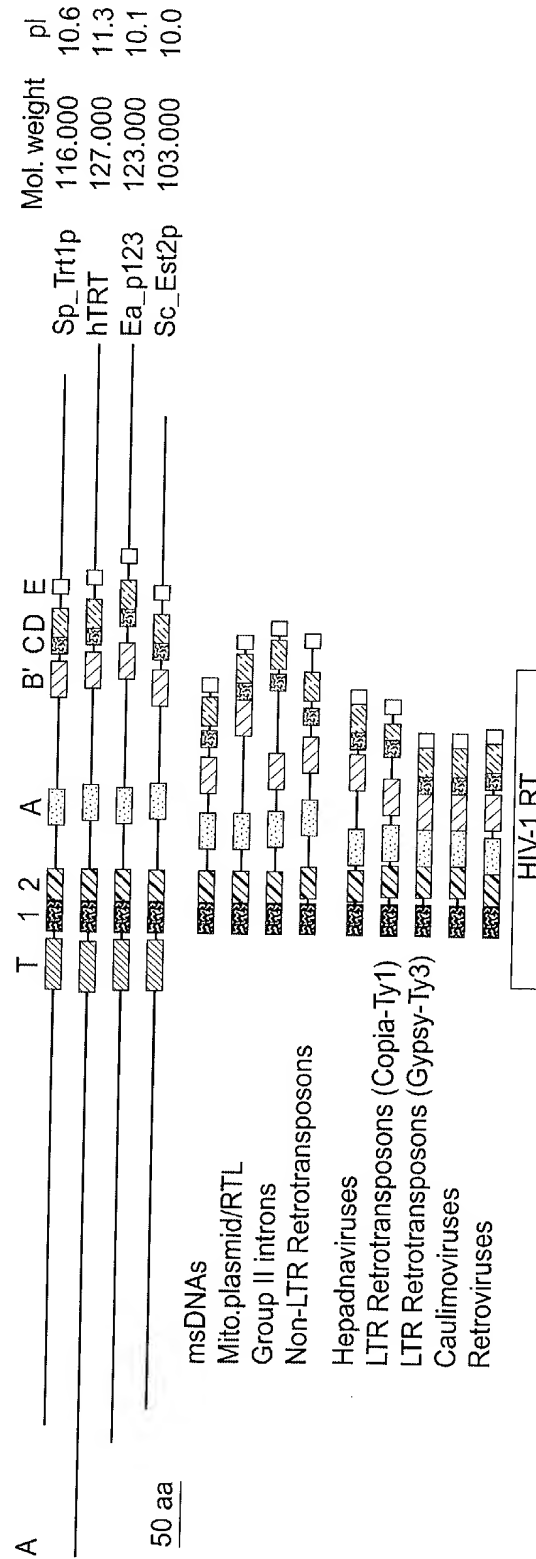
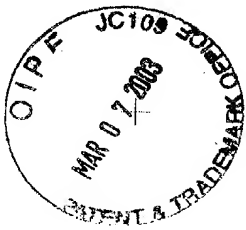


FIG. 2



3/103

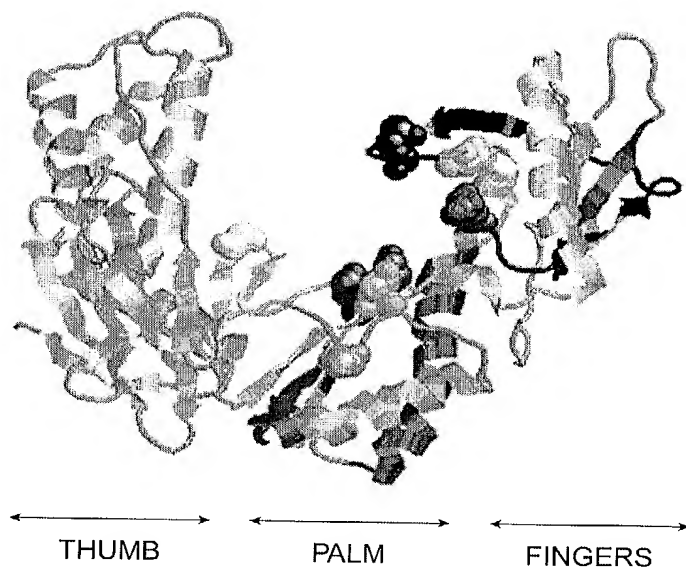


FIG. 3

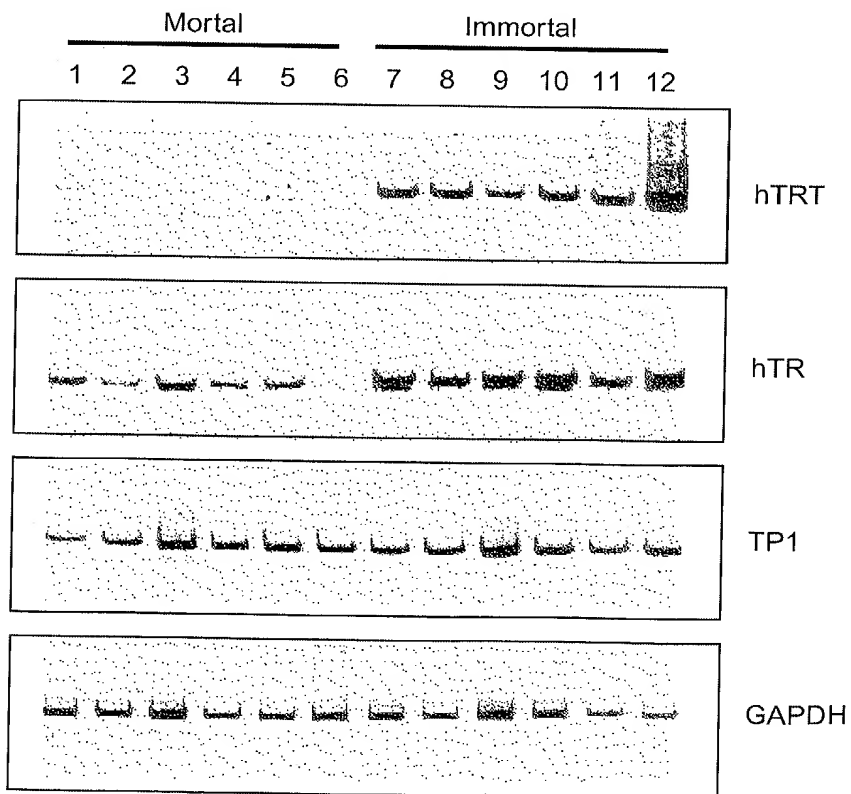


FIG. 5

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[illegible]

FIG. 4





5/103

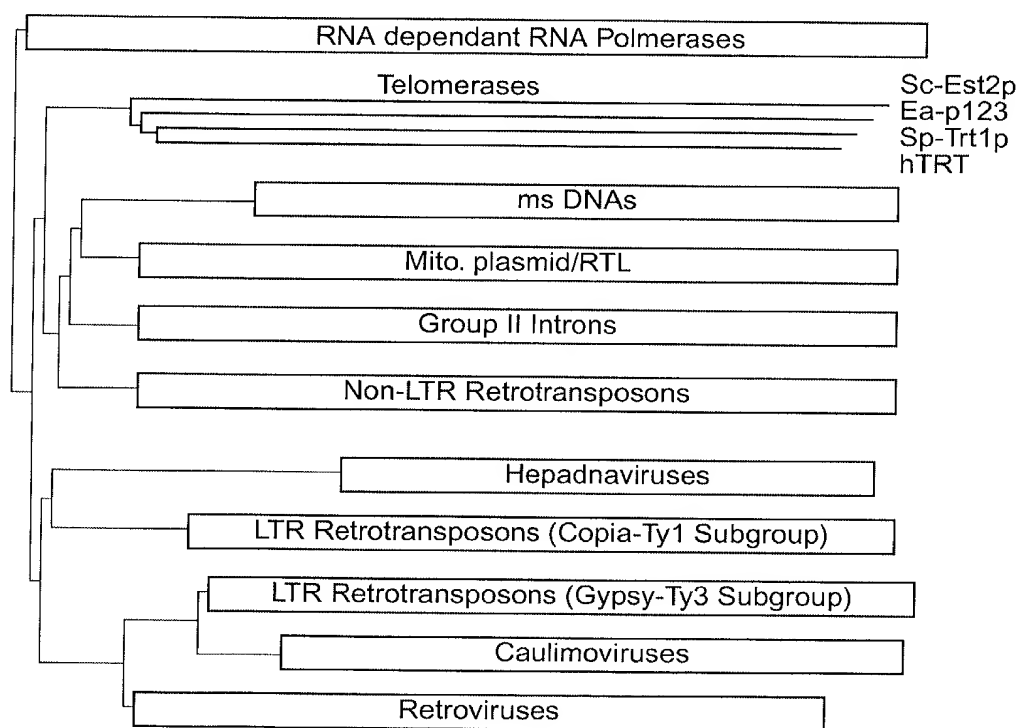


FIG. 6

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6/103

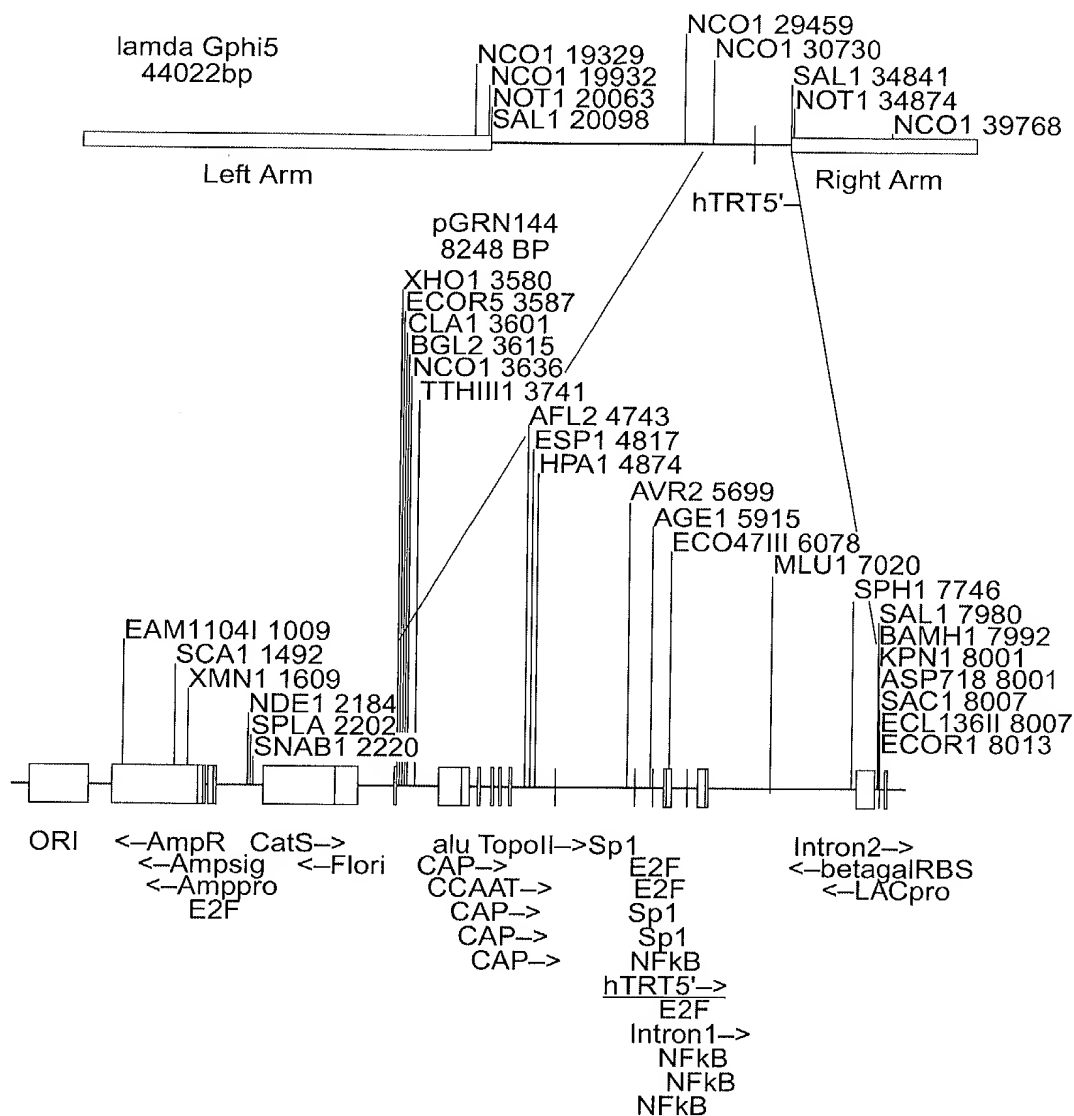
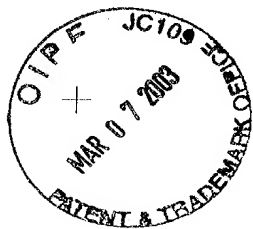


FIG. 7



7/103

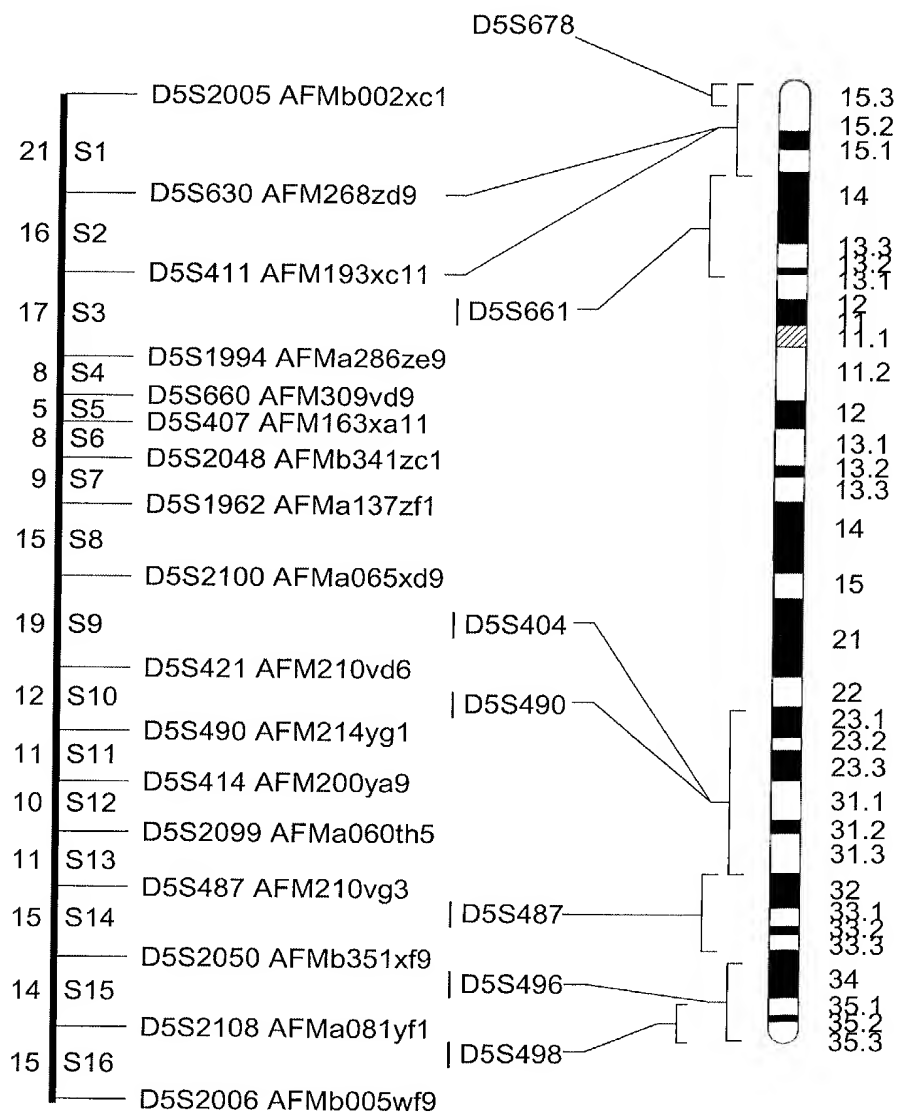


FIG. 8



8/103

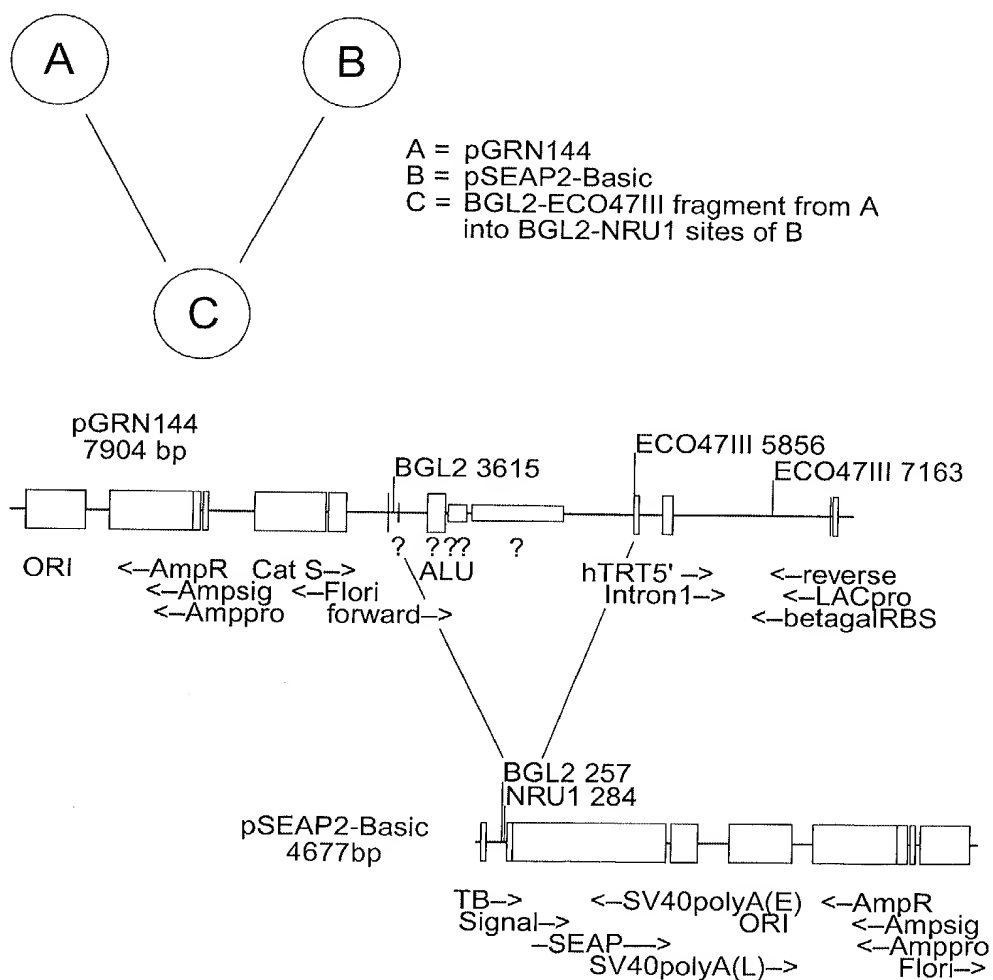
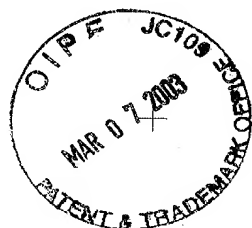


FIG. 9



9/103

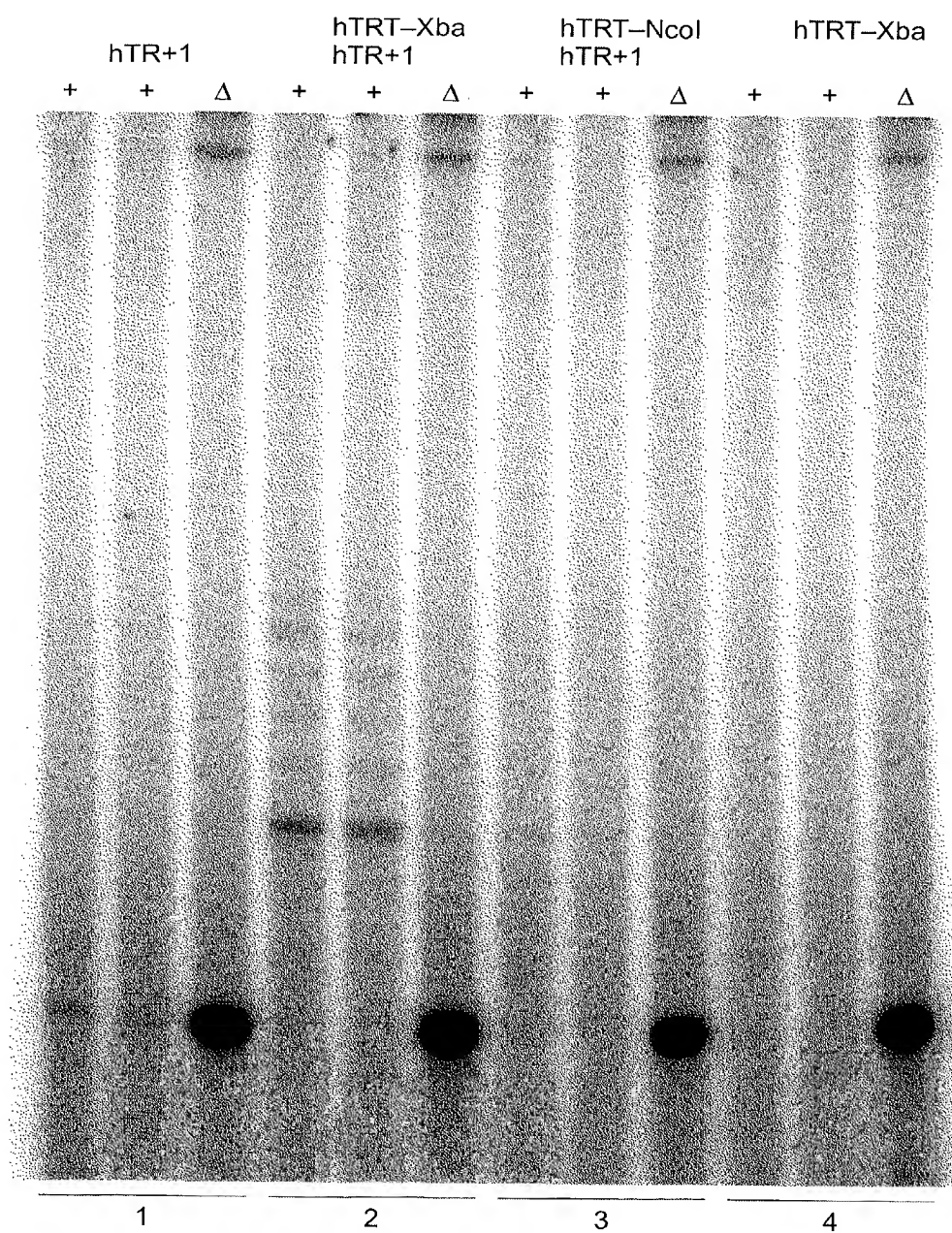


FIG. 10A

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10/103

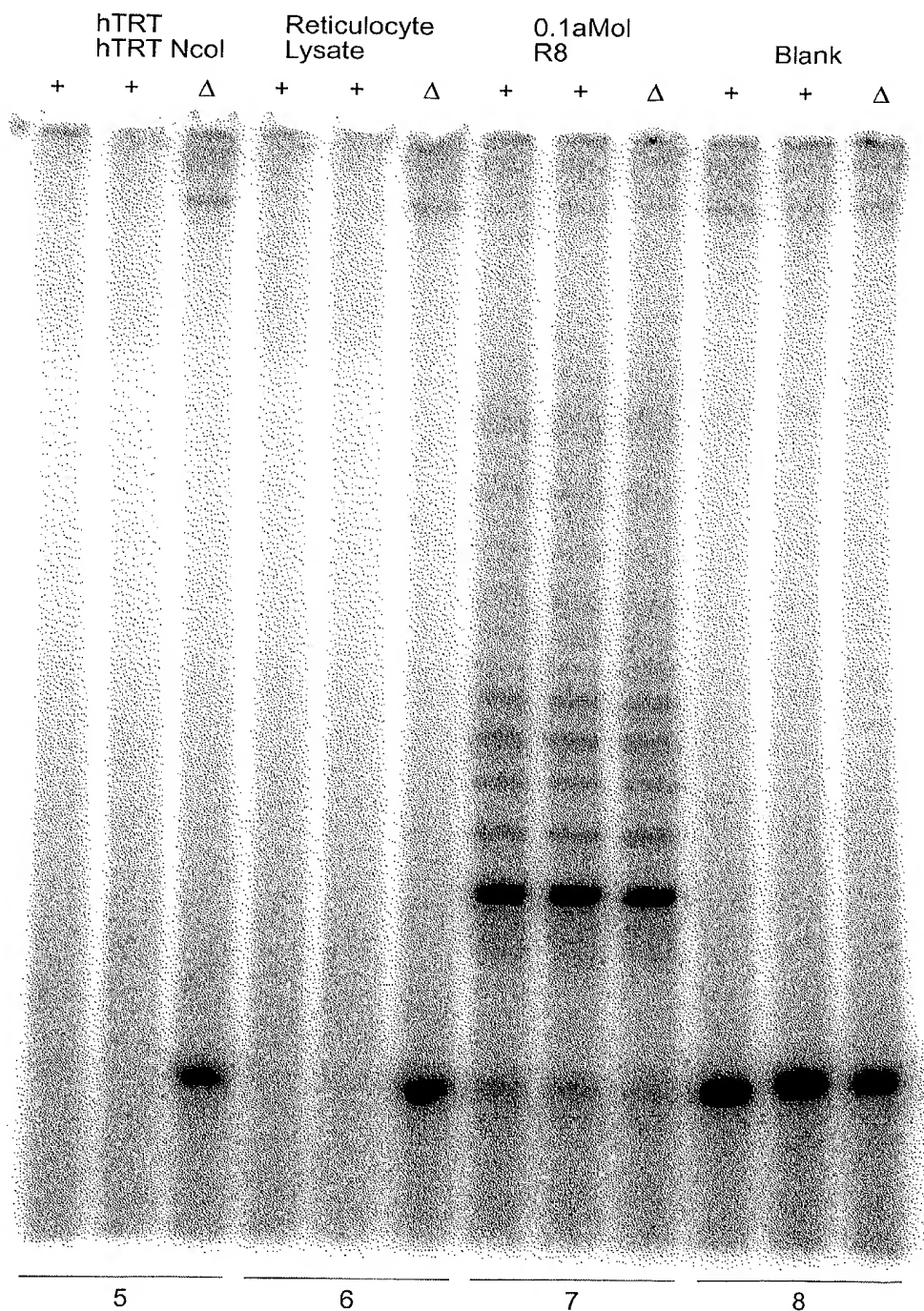


FIG. 10B

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11/103

### Telomerase Specific Motifs

TRT con	W1	MOTIF T		MOTIF T'
hTRT	546	W1MSVVVVELLRSSFFVVTETTFQKNRLFYRKSWSKLQSIGI	y Rk W 1 I	E V
spTRT	429	W1NSFIPIILQSFYITESSDLNRNRTVYFRKDIWKLICRPFI		13 EAEVR
Ea_p123	441	W1FEDLVVSLIRCFYFVTEQQKSYKTYRKNINWVIMKMSI		12 ENNVR
Sc_Est2	366	W1FRQLIPKIIQTFFCYCTEISSTVT.IVYFRHDTWKNLITPFI		12 EKEVE
				9 ENNVC

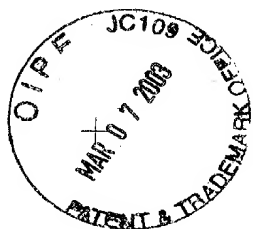
### Telomerase RT Motifs (Fingers)

TRT con	MOTIF 1	MOTIF 2	MOTIF A	MOTIF B'
hTRT	R ipKk	fr I	p lyF D cYD i	y q GiPQGs 1S 1 Y
spTRT	11 SRLRFIPKPDG 0 LRPIV	69 PELYFVKVDVTGAYDTI	104 YVQCQGIPOGSILSTLLCSLCY	
Ea_p123	10 AVIRLLPKKNT 0 FRLIT	66 RKKYFVRIDIKSCYDRI	99 YLQKVGIPQGSILSSFLCHFYM	
Sc_Est2	10 GKRLIPKKT 0 FRPIM	67 PKLFFATMDIEKCYDSV	117 YKQTKGIPQGLCVSSILSSFY	
RT con	13 SKMRIIPKKS 2 FRIIA	68 PELYFMKFDVKSCYDSI	85 YIREDGLFQGSLSAPIVDLVY	
	p hh h K	h hDh AF h	hPQG pP hh h	
		GY		

### Telomerase RT Motifs (Palm, Primer Grip)

TRT con	MOTIF C	MOTIF D	MOTIF E
hTRT	111rl DDfL it	g n K	w g s 1
spTRT	15 LLLRLVDDFLVLT 15 GVPEYGCVVNLKRTVV	24 WCGLLDTRTL	192
Ea_p123	16 VLLRVVDDFLFIT 15 GFELHNFSTSLKTVI	22 FFGFSVNMRSI	176
Sc_Est2	24 LLMRLTDDYLLIT 15 VSRENGFKFNKKLQT	28 WIGISIDMKTL	174
RT con	18 LILKLADDFLIIS 15 GFQKYNKANRDKILA	25 WKHSSTNNFH	141
	h Y DDh h	Gh h cK h	hLG h
	F		

FIG. 11



12/103

181 GGACCCGGCGGCTTTCCGCGCGCTGGTGGCCAGTGCCTGGTGTGCGTGCCCTGGGACGC  
CCTGGGCCGCCGAAAGGCGCGGACCACCGGGTCACGGACCACACGCACGGGACCCTGCG

NFkB\_CS1  
GGGRQTYTQC  
NFkB-MHC-I.2  
TGGGCTTCCCC

241 ACGGCCGCCCCCGCCGCCCCCTCCTTCCGCCAGGTGGGCCTCCCCGGGGTCGGCGTCCG  
TGCCGGCGGGGGCGGCGGGGGAGGAAGGCGGTCCACCCGAGGGGGCCCAGCCGCAGGC

Intron1

301 GCTGGGGTTGAGGGCGGCCGGGGGAACCAGCGACATGCGGAGAGCAGCGCAGGCGACTC  
CGACCCCAACTCCCGCCGGCCCCCTTGGTCGCTGTACGCCTCTCGTCGCGTCCGCTGAG

NFkB\_CS1  
GGGRQTYTQC  
NFkB\_CS2  
RGGGRMTYYCC

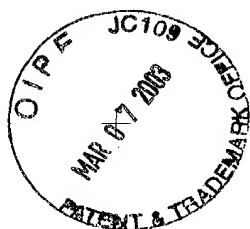
Topo\_II\_cleavage\_site  
RNYNNCNGYNGKTNINY

361 AGGGCGCTTCCCCCGCAGGTGTCCTGCCTGAAGGAGCTGGTGGCCCGAGTGCTGCAGAGG  
TCCCGCAAGGGGGCGTCCACAGGACGGACTTCCTCGACCACCGGGCTCACGACGTCTCC

FIG. 12

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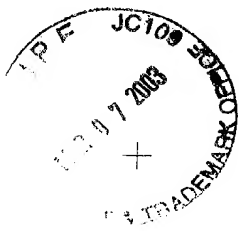




13/103

1	AAAACCCCAA	AACCCCAAAA	CCCCTTTT	AGCCCTGCAG	TTGGAAATAT
51	AACCTCAGTA	TTAATAAGCT	CAGATTTTAA	ATATTAATTA	CAAAACCTAA
101	ATGGAGGTTG	ATGTTGATAA	TCAAGCTGAT	AATCATGGCA	TTCACTCAGC
151	TCTTAAGACT	TGTGAAGAAA	TAAAGAAGC	TAAAACGTTG	TACTCTTGGA
201	TCCAGAAAGT	TATTAGATGA	AGAAATCAAT	CTCAAAGTCA	TTATAAAGAT
251	TTAGAAGATA	TTAAAATATT	TGCGCAGACA	AATATTGTTG	CTACTCCACG
301	AGACTATAAT	GAAGAAGATT	TTAAAGTTAT	TGCAAGAAAA	GAAGTATTTT
351	CAACTGGACT	AATGATCGAA	CTTATTGACA	AATGCTTAGT	TGAACCTTCTT
401	TCATCAAGCG	ATGTTTCAGA	TAGACAAAAA	CTTCAATGAT	TTGGATTTC
451	ACTTAAGGGA	AATCAATTAG	CAAAGACCCA	TTTATTAACA	GCTCTTTTCAA
501	CTCAAAAGCA	GTATTTCTTT	CAAGACGAAT	GGAACCAAGT	TAGAGCAATG
551	ATTGGAAATG	AGCTCTTCCG	ACATCTCTAC	ACTAAATATT	TAATATTCCA
601	GCGAACTTCT	GAAGGAAGCT	TTGTTCAATT	TTGCGGGAAT	AACGTTTTTG
651	ATCATTTGAA	AGTCAACGAT	AAGTTTGACA	AAAAGCAAAA	AGGTGGAGCA
701	GCAGACATGA	ATGAACCTCG	ATGTTGATCA	ACCTGCAAAAT	ACAATGTCAA
751	GAATGAGAAA	GATCACTTTC	TCAACAACAT	CAACGTGCCG	AATTGGAATA
801	ATATGAAATC	AAGAACCAGA	ATATTTTATT	GCACTCATTT	TAATAGAAAT
851	AACCAATTCT	TCAAAAAGCA	TGAGTTTGTG	AGTAACAAAA	ACAATATTTT
901	AGCGATGGAC	AGAGCTCAGA	CGATATTCAC	GAATATATTC	AGATTTAATA
951	GAATTAGAAA	GAAGCTAAAA	GATAAGGTTA	TCGAAAAAAT	TGCTTACATG
1001	CTTGAGAAAG	TCAAAGATTT	TAACCTCAAC	TACTATTTAA	CAAAATCTTG
1051	TCCTCTTCCA	GAAAATTGGC	GGGAACGGAA	ACAAAAAATC	GAAAACCTGA
1101	TAAATAAAAC	TAGAGAAGAA	AAGTCGAAGT	ACTATGAAGA	GCTGTTTAGC
1151	TACACAACTG	ATAATAAATG	CGTCACACAA	TTTATTAATG	AATTTTTCTA
1201	CAATATACTC	CCCAAAGACT	TTTTGACTGG	AAGAAACCGT	AAGAATTTTC
1251	AAAAGAAAGT	TAAGAAATAT	GTGGAACATA	ACAAGCATGA	ACTCATTAC
1301	AAAACTTAT	TGCTTGAGAA	GATCAATACA	AGAGAAATAT	CATGGATGCA
1351	GGTTGAGACC	TCTGCAAAGC	ATTTTTATTA	TTTTGATCAC	GAAAACATCT
1401	ACGCTTTATG	GAAATTGCTC	CGATGGATAT	TCGAGGATCT	CGTCGTCTCG
1451	CTGATTAGAT	GATTTTTCTA	TGTCACCGAG	CAACAGAAAA	GTTACTCCAA
1501	AACCTATTAC	TACAGAAAAG	ATATTTGGGA	CGTCATTATG	AAAATGTCAA
1551	TCGCAGACTT	AAAGAAGGAA	ACGCTTGCTG	AGGTCCAAGA	AAAAGAGGTT
1601	GAAGAATGGA	AAAAGTCGCT	TGGATTTGCA	CCTGGAAAAAC	TCAGACTAAT
1651	ACCGAAGAAA	ACTACTTTCC	GTCCAATTAT	GACTTTCAAT	AAGAAGATTG
1701	TAAATTCAGA	CCGGAAGACT	ACAAAATTAA	CTACAAATAC	GAAGTTATTG
1751	AACCTCACT	TAATGCTTAA	GACATTGAAG	AATAGAATGT	TTAAAGATCC
1801	TTTTGGATTC	GCTGTTTTTA	ACTATGATGA	TGTAATGAAA	AAGTATGAGG
1851	AGTTTGTGTT	CAAATGGAAG	CAAGTTGGAC	AACCAAAACT	CTTCTTTGCA
1901	ACTATGGATA	TCGAAAAGTG	ATATGATAGT	GTAAACAGAG	AAAACTATC
1951	AACATTCCCTA	AAAACACTA	AATTACTTTC	TTCAAGATTTT	TGGATTATGA
2001	CTGCACAAAT	TCTAAAGAGA	AAGAATAACA	TAGTTATCGA	TTCGAAAAAC
2051	TTTAGAAAAG	AAGAAATGAA	AGATTATTTT	AGACAGAAAT	TCCAGAAGAT
2101	TGCACTTGAA	GGAGGACAAT	ATCCAACCTT	ATTCAGTGTT	CTTGAAAAATG
2151	AACAAAATGA	CTTAAATGCA	AAGAAAACAT	TAATTGTTGA	AGCAAAGCAA
2201	AGAAATTATT	TTAAGAAAGA	TAACCTACTT	CAACCAGTCA	TTAATATTTG
2251	CCAATATAAT	TACATTAAC	TTAATGGGAA	GTTTTATAAA	CAAACAAAAG
2301	GAATTCCTCA	AGGTCTTTGA	GTTTCATCAA	TTTTGTGATC	ATTTTATTAT
2351	GCAACATTAG	AGGAAAGCTC	CTTAGGATTC	CTTAGAGATG	AATCAATGAA

FIG. 13



14/103

2401	CCCTGAAAAT	CCAAATGTTA	ATCTTCTAAT	GAGACTTACA	GATGACTATC
2451	TTTTGATTAC	AACTCAAGAG	AATAATGCAG	TATTGTTTAT	TGAGAAACTT
2501	ATAAACGTAA	GTCGTGAAAA	TGGATTTAAA	TTCAATATGA	AGAAACTACA
2551	GACTAGTTTT	CCATTAAGTC	CAAGCAAAT	TGCAAAATAC	GGAATGGATA
2601	GTGTTGAGGA	GCAAAATATT	GTTCAAGATT	ACTGCGATTG	GATTGGCATC
2651	TCAATTGATA	TGAAAACTCT	TGCTTTAATG	CCAAATATTA	ACTTGAGAAT
2701	AGAAGGAATT	CTGTGTACAC	TCAATCTAAA	CATGCAAACA	AAGAAAGCAT
2751	CAATGTGGCT	CAAGAAGAAA	CTAAAGTCGT	TTTTAATGAA	TAACATTACC
2801	CATTATTTTA	GAAAGACGAT	TACAACCGAA	GACTTTGCGA	ATAAACTCT
2851	CAACAAGTTA	TTTATATCAG	GCGGTTACAA	ATACATGCAA	TGAGCCAAAG
2901	AATACAAGGA	CCACTTTAAG	AAGAACTTAG	CTATGAGCAG	TATGATCGAC
2951	TTAGAGGTAT	CTAAAATTAT	ATACTCTGTA	ACCAGAGCAT	TCTTTAAATA
3001	CCTTGTGTGC	AATATTAAGG	ATACAATTTT	TGGAGAGGAG	CATTATCCAG
3051	ACTTTTTCCT	TAGCACACTG	AAGCACTTTA	TTGAAATATT	CAGCACAAAA
3101	AAGTACATTT	TCAACAGAGT	TTGCATGATC	CTCAAGGCAA	AAGAAGCAAA
3151	GCTAAAAAGT	GACCAATGTC	AATCTCTAAT	TCAATATGAT	GCATAGTCGA
3201	CTATTCTAAC	TTATTTTGGA	AAGTTAATTT	TCAATTTTTG	TCTTATATAC
3251	TGGGGTTTTG	GGGTTTTGGG	GTTTTGGGG		

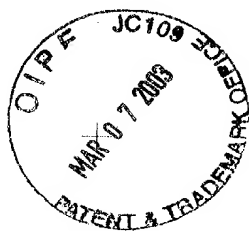
FIG. 13  
(CONTINUED)

1	MEVDVDNQAD	NHGIHSALKT	CEEIKEAKTL	YSWIQKVIRC	RNQSQSHYKD
51	LEDIKIFAQT	NIVATPRDYN	EEDFKVIARK	EVFSTGLMIE	LIDKCLVELL
101	SSSDVSDRQK	LQCFGFQLKG	NQLAKTHLLT	ALSTQKQYFF	QDEWNQVRAM
151	IGNELFRHLY	TKYLIFQRTS	EGTLVQFCGN	NVFDHLKVND	KFDKKQKGGGA
201	ADMNEPRCCS	TCKYNVKNEK	DHFLNNINVP	NWNNMKSRT	IFYCTHFNRN
251	NQFFKKHEFV	SNKNNISAMD	RAQTIFTNIF	RFNRIRKKLK	DKVIEKIAM
301	LEKVKDFNFN	YYLTKSCPLP	ENWRERKQKI	ENLINKTREE	KSKYYEELFS
351	YTNDNKCVTQ	FINEFFYNIL	PKDFLTGRNR	KNFQKKVKKY	VELNKHELH
401	KNLLEKINT	REISWMQVET	SAKHFFYYFDH	ENIYVLWKKL	RWIFEDLVVS
451	LIRCFYVTE	QKSYSKTYE	YRKNWDVIM	KMSIADLKKE	TLAEVQEKEV
501	EEWKSLGFA	PGKLRLIPKK	TTERPIMTFN	KKIVNSDRKT	TKLTTNTKLL
551	NSHMLKTLK	NRMFKDPFGF	AVFNYDDVMK	KYEEFVCKWK	QVGQPKLFFA
601	TMDIEKCYDS	VNREKLSTFL	KTTKLLSSDF	WIMTAQILKR	KNNIVIDSKN
651	FRKKEMKDYF	RQKFQKIALE	GGQYPTLFSV	LENEQNDLNA	KKTLIVEAKQ
701	RNYFKKDNLL	QPVINICQYN	YINFNGKFYK	QTKGIPQGLC	VSSILSSFYY
751	ATLEESSLGF	LRDESMNPEN	PNVNLLMRLT	DDYLLITTQE	NNAVLFIEKL
801	INVSRENGFK	FNMKKLQTSF	PLSPSKFAKY	GMDSVEEQNI	VQDYCDWIGI
851	SIDMKTLALM	PNINLRIEGI	LCTLNLNMQT	KKASMWLKKK	LKSFLMNNIT
901	HYFRKTITTE	DFANKTLNKL	FISGGYKYM	CAKEYKDHFK	KNLAMSSMID
951	LEVSKIIYSV	TRAFFKYLVC	NIKDTIFGEE	HYPDFFLSTL	KHFIEIFSTK
1001	KYIFNVRVCM	LKAKEAKLKS	DQCQSLIQYD	A	

FIG. 14

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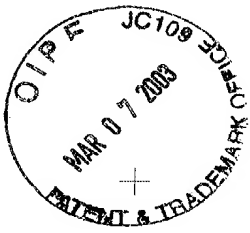


16/103

1470 GAT CTC GTT TCT ACT TTT CCT AAT TAC CTT ATA TCT ATA CTT GAG TCA AAA AAT TGG CAA 1529  
129 D L V S T F P N Y L I S I L E S K N W Q 148  
1530 CTT TTG TTA GAA AT gtaatatccgggttaagatgttgccgactttgaacaagactgacaagtatag T ATC GGC 1601  
149 L L L E I I G 155  
1602 AGT GAT GCC ATG CAT TAC TTA TTA TCC AAA GGA AGT ATT TTT GAG GCT CTT CCA AAT GAC 1661  
156 S D A M H Y L L S K G S I F E A L P N D 175  
1662 AAT TAC CTT CAG ATT TCT GGC ATA CCA CTT TTT AAA AAT AAT GTG TTT GAG GAA ACT GTG 1721  
176 N Y L Q I S G I P L F K N N V F E E T V 195  
1722 TCA AAA AAA AGA AAG CGA ACC ATT GAA ACA TCC ATT ACT CAA AAT AAA AGC GCC CGC AAA 1781  
196 S K K R K R T I E T S I T Q N K S A R K 215  
1782 GAA GTT TCC TGG AAT AGC ATT TCA ATT AGT AGG TTT AGC ATT TTT TAC AGG TCA TCC TAT 1841  
216 E V S W N S I S I S R F S I F Y R S S Y 235  
1842 AAG AAG TTT AAG CAA G gtaactaactgtttatccttcataactaatttttag AT CTA TAT TTT AAC 1907  
236 K K F K Q D L Y F N 245  
1908 TTA CAC TCT ATT TGT GAT CGG AAC ACA GTA CAC ATG TGG CTT CAA TGG ATT TTT CCA AGG 1967  
246 L H S I C D R N T V H M W L Q W I F P R 265  
1968 CAA TTT GGA CTT ATA AAC GCA TTT CAA GTG AAG CAA TTG CAC AAA GTG ATT CCA CTG GTA 2027  
266 Q F G L I N A F Q V K Q L H K V I P L V 285  
2028 TCA CAG AGT ACA GTT GTG CCC AAA CGT CTC CTA AAG GTA TAC CCT TTA ATT GAA CAA ACA 2087  
286 S Q S T V V P K R L L K V Y P L I E Q T 305  
2088 GCA AAG CGA CTC CAT CGT ATT TCT CTA TCA AAA GTT TAC AAC CAT TAT TGC CCA TAT ATT 2147  
306 A K R L H R I S L S K V Y N H Y C P Y I 325  
2148 GAC ACC CAC GAT GAT GAA AAA ATC CTT AGT TAT TCC TTA AAG CCG AAC CAG GTG TTT GCG 2207  
326 D T H D D E K I L S Y S L K P N Q V F A 345  
2208 TTT CTT CGA TCC ATT CTT GTT CGA GTG TTT CCT AAA TTA ATC TGG GGT AAC CAA AGG ATA 2267  
346 F L R S I L V R V F P K L I W G N Q R I 365

FIG. 15  
(CONTINUED)

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17/103

2268 TTT GAG ATA ATA TTA AAA G gttattgtataaaattttattaccactaacgattttaccag AC CTC GAA ACT 2336  
366 F E I I L K D L E T 375

2337 TTC TTG AAA TTA TCG AGA TAC GAG TCT TTT AGT TTA CAT TAT TTA ATG AGT AAC ATA AAG 2396  
376 F L K L S R Y E S F S L H Y L M S N I K 395

2397 gtaatatgccaaattttttaccatttaataacaatcag ATT TCA GAA ATT GAA TGG CTA GTC CTT GGA 2465  
396 I S E I E W L V L G 405

2466 AAA AGG TCA AAT GCG AAA ATG TGC TTA AGT GAT TTT GAG AAA CGC AAG CAA ATA TTT GCG 2525  
406 K R S N A K M C L S D F E K R K Q I F A 425

2526 GAA TTC ATC TAC TGG CTA TAC AAT TCG TTT ATA ATA CCT ATT TTA CAA TCT TTT TTT TAT 2585  
426 E F I Y W L Y N S F I I P I L Q S F F Y 445

2586 ATC ACT GAA TCA AGT GAT TTA CGA AAT CGA ACT GTT TAT TTT AGA AAA GAT ATT TGG AAA 2645  
446 I T E S S D L R N R T V Y F R K D I W K 465

2646 CTC TTG TGC CGA CCC TTT ATT ACA TCA ATG AAA ATG GAA GCG TTT GAA AAA ATA AAC GAG 2705  
466 L L C R P F I T S M K M E A F E K I N E 485

2706 gtatttttaaagtattttttgtcaaaaagctaatttttcag AAC AAT GTT AGG ATG GAT ACT CAG AAA ACT 2775  
486 N N V R M D T Q K T 495

2776 ACT TTG CCT CCA GCA GTT ATT CGT CTA TTA CCT AAG AAG AAT ACC TTT CGT CTC ATT ACG 2835  
496 T L P P A V I R L L P K K N T F R L I T 515

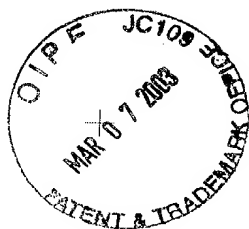
2836 AAT TTA AGA AAA AGA TTC TTA ATA AAG gtatttaatttttggtcacatgaatgtactttcattcattatta 2906  
516 N L R K R F L I K 524

2907 ttagcag ATG GGT TCA AAC AAA AAA ATG TTA GTC AGT ACG AAC CAA ACT TTA CGA CCT GTG 2967  
525 M G S N K K M L V S T N Q T L R P V 542

2968 GCA TCG ATA CTG AAA CAT TTA ATC AAT GAA GAA AGT AGT GGT ATT CCA TTT AAC TTG GAG 3027  
543 A S I L K H L I N E E S S G I P F N L E 562

3028 GTT TAC ATG AAG CTT ACT TTT AAG AAG GAT CTT CTT AAG CAC CGA ATG TTT GG gtaat 3088  
563 V Y M K L L T F K K D L L K H R M F G 581

FIG. 15  
(CONTINUED)



18/103

3089 tatataatgcgcgattcctcattattaattttgcag G CGT AAG AAG TAT TTT GTA CGG ATA GAT ATA 3155  
582 R K K Y F V R I D I 591

3156 AAA TCC TGT TAT GAT CGA ATA AAG CAA GAT TTG ATG TTT CGG ATT GTT AAA AAG AAA CTC 3215  
592 K S C Y D R I K Q D L M F R I V K K L 611

3216 AAG GAT CCC GAA TTT GTA ATT CGA AAG TAT GCA ACC ATA CAT GCA ACA AGT GAC CGA GCT 3275  
612 K D P E F V I R K Y A T I H A T S D R A 631

3276 ACA AAA AAC TTT GTT AGT GAG GCG TTT TCC TAT T gtaagtttttttttcattggaattttttaacaa 3343  
632 T K N F V S E A F S Y F 643

3344 atttttttttag TT GAT ATG GTG CCT TTT GAA AAA GTC GTG CAG TTA CTT TCT ATG AAA ACA 3405  
644 D M V P F E K V V Q L L S M K T 659

3406 TCA GAT ACT TTG TTT GTT GAT TTT GTG GAT TAT TGG ACC AAA AGT TCT TCT GAA ATT TTT 3465  
660 S D T L F V D F V D Y W T K S S E I F 679

3466 AAA ATG CTC AAG GAA CAT CTC TCT GGA CAC ATT GTT AAG gtataccaattgtgaattgtaataaca 3532  
680 K M L K E H L S G H I V K 692

3533 ctaatgaaactag ATA GGA AAT TCT CAA TAC CTT CAA AAA GTT GGT ATC CCT CAG GGC TCA 3593  
693 I G N S Q Y L Q K V G I P Q G S 708

3594 ATT CTG TCA TCT TTT TTG TGT CAT TTC TAT ATG GAA GAT TTG ATT GAT GAA TAC CTA TCG 3653  
709 I L S S F L C H F Y M E D L I D E Y L S 728

3654 TTT ACG AAA AAG AAA GGA TCA GTG TTG TTA CGA GTA GTC GAC GAT TTC CTC TTT ATA ACA 3713  
729 F T K K K G S V L L R V V D D F L F I T 748

3714 GTT AAT AAA AAG GAT GCA AAA AAA TTT TTG AAT TTA TCT TTA AGA G gtgagttgctgcattcc 3777  
749 V N K K D A K K F L N L S L R G 764

3778 taagttctaacccgttgaag GA TTT GAG AAA CAC AAT TTT TCT ACG AGC CTG GAG AAA ACA GTA 3840  
765 F E K H N F S T S L E K T V 778

3841 ATA AAC TTT GAA AAT AGT AAT GGG ATA ATA AAC AAT ACT TTT TTT AAT GAA AGC AAG AAA 3900  
779 I N F E N S N G I I N N T F F N E S K K 798

FIG. 15  
(CONTINUED)

3901 AGA ATG CCA TTC TTC GGT TTC TCT GTG AAC ATG AGG TCT CTT GAT ACA TTG TTA GCA TGT 3960  
799 R M P F F G F S V N M R S L D T L L A C 818

3961 CCT AAA ATT GAT GAA GCC TTA TTT AAC TCT ACA TCT GTA GAG CTG ACG AAA CAT ATG GGG 4020  
819 P K I D E A L F N S T S V E L T K H M G 838

4021 AAA TCT TTT TTT TAC AAA ATT CTA AG gtatactgtgtaactgaataatagctgacaaaataatcag A TCG 4089  
839 K S F Y K I L R S 848

4090 AGC CTT GCA TCC TTT GCA CAA GTA TTT ATT GAC ATT ACC CAC AAT TCA AAA TTC AAT TCT 4149  
849 S L A S F A Q V F I D I T H N S K F N S 868

4150 TGC TGC AAT ATA TAT AGG CTA GGA TAC TCT ATG TGT ATG AGA GCA CAA GCA TAC TTA AAA 4209  
869 C C N I Y R L G Y S M C M R A Q A Y L K 888

4210 AGG ATG AAG GAT ATA TTT ATT CCC CAA AGA ATG TTC ATA ACG G gtgagtacttattttaactaga 4274  
889 R M K D I F I P Q R M F I T D 903

4275 aaagtcattaattaaccttag AT CTT TTG AAT GTT ATT GGA AGA AAA ATT TGG AAA AAG TTG GCC 4339  
904 L L N V I G R K I W K K L A 917

4340 GAA ATA TTA GGA TAT ACG AGT AGG CGT TTC TTG TCC TCT GCA GAA GTC AAA TG gtacgtgtc 4401  
918 E I L G Y T S R R F L S S A E V K W 935

4402 ggtctcgagacttcagcaaatattgacacatcag G CTT TTT TGT CTT GGA ATG AGA GAT GGT TTG AAA 4468  
936 L F C L G M R D G L K 946

4469 CCC TCT TTC AAA TAT CAT CCA TGC TTC GAA CAG CTA ATA TAC CAA TTT CAG TCA TTG ACT 4528  
947 P S F K Y H P C F E Q L I Y Q F Q S L T 966

4529 GAT CTT ATC AAG CCG CTA AGA CCA GTT TTG CGA CAG GTG TTA TTT TTA CAT AGA ATA 4588  
967 D L I K P L R P V L R Q V L F L H R I 986

4589 GCT GAT TAA tgtcattttcaatttattatatacatccctttattactggtgttttaacaataattattactaagtata 4665  
987 A D \* 989

FIG. 15  
(CONTINUED)

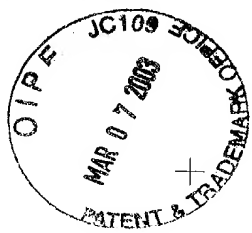


20/103

4666 gctgacccccaaagcaagcactataggtttcttagtaaaagtaaaataatctcgttattagttttgatgacttgtct 4745  
4746 ttatccttatacttttaagaaagattgacagtgggtgctgactactgccacatgcccatcaacgggagtggttaaca 4825  
4826 ttaaaagtaatacatgaggttaattccttctatttagaataaggaaagtgggtttctataatgaataatgccgcacta 4905  
4906 atgcaaaaagacgaagattatcttcaaaagggggttaagcatatccgaaggaaagagagtaataataccagtggt 4985  
4986 gttgaagaaagcaaggataatttggaacaaagcttctgcagatgacaggctaaattttggtgacccgaattttggtaaaagc 5065  
5066 ccagggtatccatgggtggccggccttgcctactgagacgaaagaaactaaggatagtttgaataactaataatagctcat 5145  
5146 atgtcttataaagggttttgggttttctgacttcaattttgcatgggtgaaagaaatagtttaagccattattggat 5225  
5226 tccgaaatagccaaatttcttgggttccctcaagcggaagtctaagaacttattgaagcttatgaggttcaaaaaactcc 5305  
5306 tcctgatttaaggagggaatcttccacccgatgaggaaatggatagcttaccgctgctgaggagagaagccctaatttttgc 5385  
5386 aaaaaagaaaatatcatgggagacatctcttgatgaatcagatgaggagagatctccagcggtatccttgatgtcaata 5465  
5466 acttctatttctgaaatgtatgggtcctactgtcgcttcgacttctcgtagtctctacgcagtttaagtgacccaaaggtagc 5544

FIG. 15  
(CONTINUED)





21/103

1 gcagcgctgc gtcctgetgc gcacgtggga agccctggcc ccggccaccc ccgcgatgoc  
61 gcgcgctccc cgctgccgag ccgtgcgctc cctgctgcgc agccactacc gcgaggtgct  
121 gccgctggcc acgttcctgc ggccgctggg gccccagggc tggcggtcg tgcagcgcg  
181 ggaccogggc gctttccgcg cgctgggtgg ccagtgcctg gtgtgcgtgc cctgggacgc  
241 acggccgccc cccgcccggc cctccttccg ccaggtgtcc tgccctgaagg agctgggtggc  
301 ccgagtgtcg cagaggtgtg gcgagcgcg cggaagaac gtgctggcct tcggcttcgc  
361 gctgctggac gggggcccg ggggcccccc cgaggccttc accaccagcg tgcgcagcta  
421 cctgcccac acggtgaccg acgcactgcg ggggagcggg gcgtgggggc tgctgtgcg  
481 ccgctggggc gacgacgtgc tggttcacct gctggcacgc tgcgcgtct ttgtgctgg  
541 ggctcccagc tgcgcctacc aggtgtgcgg gccgcgctg taccagctcg gcgtgccac  
601 tcaggcccg ccccgccac acgctagtgg accccgaagg cgtctgggat gcgaacgggc  
661 ctggaacat agcgtcaggg aggcgggggt cccctgggc ctgccagccc cgggtgcgag  
721 gaggcgcggg ggcagtgcc a gccaagtct gccgttgccc aagaggccca ggcgtggcg  
781 tgccccagag ccggagcgga cgcccggttg gcaggggtcc tggggccacc cgggcaggac  
841 gcgtggaccg agtgaccgtg gtttctgtg ggtgtcacct ggcgtcgga gccagaagc  
901 cactctttt gaggggtgcg tctctggcac gcgcaactcc caccatccg tgggcccga  
961 gcaccacgc ggcccccat ccacatcgcg gccacacgt cactcctca ggcgacaagg agcagctgcg  
1021 cccggtgtac gccagagcca agcactcct ctctgaggcc cagcctgact ggctcgctga  
1081 gccctccttc ctactcagct ctctgaggcc ggcctggat gccagggact ccccgaggt  
1141 gaccatcttt ctgggttcca tgcggccctt gtttctggag ctgcttggga accaccgca  
1201 gccccagcg tactggcaaa ggggtgctcc tgcgcccgcg cgagctgcgg ccgaagaagc  
1261 gtcgcccac ggggtgctcc tgtgcccggg gggctctgtg gcggcccccg agggaggga  
1321 agccggtgtc cgtcgctgg cgtcgctgg tgcagctgct ccgcccagc agcagcccc  
1381 cacagacccc cgggcttctg cggcctgccc tgcgcccggc ggtgccccca ggccctctggg  
1441 cggcttctg cgggcttctg ggaacaccaa gaagttcatc tccctgggga agcatgccaa  
1501 caacgaacgc cgttcttca cgtggaagat gagcgtgcgg gactgcgctt ggctgcgag  
1561 gctctcgctg gttggctgtg ttccggccgc agagcacctg ctgctgagg agatcctggc  
1621 gagcccaggg cactggctga tgagtgtga cgtcgtcgag ctgctcaggt ctttcttta  
1681 caagtccctg accacgtttc aaaagaacag gctctttttc taccggaaga gtgtctggag  
1741 tgtaacggag agcattggaa tcagacagca cttgaagagg gtgcaactgc gggagctgtc  
1801 caagtgtcaa gtcaggcag atcggaagc caggccccgc ctgctgactg ccagactccg  
1861 ggaagcagag gtcaggcag ggtcgcggcc gattgtgaac atggactacg tcgtgggagc  
1921 cttcatcccc cgcagagaaa agagggccga gcgtctcacc tccgaggtga aggcactgtt  
1981 cagaacgttc aactacgagc gggcgccggc ccccgccctc ctggggcctc cgtgtgcgg  
2041 cagcgtgtc atccacagg cctggtgctg tctcgtgctg cgtgtgcggg ccaggacccc  
2101 cctggacgat ctgtactttg tcaaggtgga tgtgacgggc gcgtacgaca ccatccccc  
2161 gccgctgag acggaggtca togccagcat catcaaacc cagaacacgt actgcgtgcg  
2221 ggacaggctc gtgggtccaga aggcgcgcca tgggcacgtc cgcaaggcct tcaagagcca  
2281 tcggtatgoc ttgacagacc cccagcgta catgacagag ttcgtggctc acctgcagga  
2341 cgtctctacc ctgagggatg ccgtcgtcct cgagcagagc tccctcctga atgaggccag  
2401 gaccagcccc ttgcagctct tectacgctt catgtgccac cagcgcgtg gcactcagggg  
2461 cagtggcctc gtccagtgc aggggatccc gcagggctcc atccttcca cgtgctctg  
2521 caagtctac gtcggcgaca tggagaacaa gctgtttgcg gggattcggc gggaggggt  
2581 cagcctgtgc ttggtggatg atttcttgtt ggtgacacct cacctcacc cactgcagat  
2641 gctcctgcgt accctggtec gaggtgtccc tgagtatggc tgcgtggatg acttgccgaa  
2701 cttcctcagg aacttccctg tagaagacga ggccctgggt ggcaaggctt ttgttcagat  
2761 gacagtggg aacttccctg cctggtgcgg cctgctgctg gatacccgga cctggaggt  
2821 gccggccccc ggcctattcc atgcccggac ctccatcaga gccagtctca ccttcaacg  
2881 gcagagcgac tactccagct agcagcgagc caaactcttt ggggtcttgc ggcgtgaagt  
2941 cggcttcaag gctgggagga acatgcgtcg tgcaggtgaa acggtgtgca ccaacatcta  
3001 tcacagcctg tttctggatt tgcaggtgaa tcaagcatgt gtgctgcagc tccatttca  
3061 caagatcctc ctgctgcagg cgtacaggtt ccacattttt cctgcgcgtc atctctgaca cggcctccc  
3121 tcagcaagtt atcctgaaag ccaagaacgc agggatgtcg ctgggggcca agggcgccg  
3181 ctgctactcc cctccgagg ccgtgcagtg gctgtgccac caagcattcc tgotcaagct  
3241 cggccctctg cctccgagg acgtgccact cctggggctca ctcaggacag ccagacgca  
3301 gactcgacac aagctcccgg gacgacgct gactgcctg gaggccgag ccaacccggc  
3361 gctgagtcgg gacttcaaga ccacctctgga ctgatggcca gccgccaca cccaggccga  
3421 actgocctca cagcagccct gtcacgcgg gctctacgtc ccagggaggg aggggccc  
3481 gagcagacac cccgaccgc tgggagctg aggcctgagt gactgtttgg ccgagggctg  
3541 cacaccagg cccgaccgc tgggagctg aggcctgagt gactgtttgg ccgagggctg  
3601 catgtccggc tgaaggctga gtgtccggt gaggcctgag cgagtgtcca gccaaaggct  
3661 gagtgtccag cacacctgc gtcttcaact cccacaggc tggcgctcgg ctcacccca  
3721 gggccagctt ttctcacca ggagccggc ttccactccc cactataggaa tagtccatcc  
3781 ccagatctgc cattgttca cctcctccc gcctccttt cactataggaa tagtccatcc  
3841 aggtggagac cctgagaagg accctgggag ctctgggaat tggagtgac caaagggtg  
3901 cctgtacac aggcgaggac cctgcacct gatgggggtc cctgtgggtc aaattggggg  
3961 gaggtgctgt gggagtaaaa tactgaatat atgagttttt cagttttgaa aaaaa

FIG. 16

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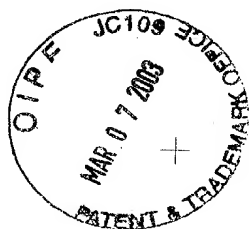
22/103

MPRAPRCRAVRSLLRSHYREVLPLATFVRRLLGPQGWRLVQRGDP  
AAFRALVAQCLVCVPWDARPPPAAPSFRQVSCIKEIVARVLQRL  
CERGAKNVLAFGFALLDGARGGPPEAFTTSVRSYLPNTVTDALR  
GSGAWGLLLRRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPLY  
QLGAATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPG  
ARRRGGSASRSPLPKRPRRGAAPEPERTPVGQGSWAHPGRTRG  
PSDRGFCVVSPPARPAEEATSLEGALSGTRHSHPSVGRQHHAGPP  
STSRPPRPWDTPCPPVYAETKHFLYSSGDKEQLRPSFLLSSLRP  
SLTGARRLVETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLEL  
LGNHAQCPYGVLLKTHCPLRAAVTPAAGVCAREKPPQGSVAAPPEE  
EDTDPRRLVQLLRQHSSPWQVYGFVRACLRRLVPPGLWGSRHNE  
RRFLRNTKKFISLGKHAKLSLQELTWKMSVRDCAWLRSPGVGC  
VPAAEHRLREEILAKFLHWMMSVYVVELLRSFFYVTETTQKNR  
LFFYRKSVWSKLQSIGIRQHLKRVQLRELSEAEVRQHREARPAL  
LTSRLRFIPKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVKA  
LFSVLNRYERARRPGLLGASVGLDDIHRARWTFVLRVRAQDPPP  
ELYFVKVDVTGAYDTIPQDRLTEVIASIIKPONTYCVRRYAVVQ  
KAAHGHRKAFKSHVSTLTDLPYMRQFVAHLQETSPLRDAVVI  
EQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSYVQCQGIPOGSI  
LSTLLCSLCYGD MENKLFAGIRRDGLLLRLVDDFLLVTPHLTHA  
KTFRLTLVRGVPEYGCVVNLKRTVVNFPVEDEALGGTAFVQMPA  
HGLFPWCGLLLDTRTLEVQSDYSSYARTSIRASLTFNRGFKAGR  
NMRRKLFGLRLKCHSLFLDLQVNSLQTVCTNIYKILLLQAYRF  
HACVLQLPFHQVWKNPTFFLRVISDTASLCYSILKAKNAGMSL  
GAKGAAGPLPSEAVQWLCHQAFLLKLTRHRVTYVPLLGLSLRTAQ  
TQLSRKLPGTTLTALEAAANPALPSDFKTIID

FIG. 17

GGCCAAGTTCCTGCACTGGCTGATGAGTGTGTACGTCGTCGAGCTGCTCAGGTCTTTCTT  
TTATGTACAGGAGACCAGTTTCAAAGAACAGGCTCTTTTCTACCGGAAGAGTGTCTG  
GAGCAAGTTGCAAAGCATTGGAATCAGACAGCACTTGAAGAGGGTGACGTCGCGGAGCT  
GTCGGAAGCAGAGGTGAGGACGATCGGGAAGCCAGGCCCGCCCTGCTGACGTCAGACT  
CCGCTTCATCCCCAAGCCTGACGGGCTGCGGCCGATTGTGAACATGGACTACGTCGTGGG  
AGCCAGAACGTTCCGCAGAGAAAAGAGGGCCGAGCGTCTCACCTCGAGGGTGAAAGCACT  
GTTACGCGTGCTCAACTACGAGCGGGCGCGGCCCGCCCTCCTGGGCGCCTCTGTGCT  
GGGCTTGACGATATCCACAGGGCCTGGCGCACCTTCGTGCTGCGTGTGCGGGCCAGGA  
CCCGCCGCTGAGCTGTACTTTGTCAAGGTGGATGTGACGGGCGGTACGACACCATCCC  
CCAGGACAGGCTCACGGAGGTGATCGCCAGCATCATCAAACCCAGAACACGTACTGCGT  
GCGTCGGTATGCGGTGGTCCAGAAGGCCGCCCATGGGCACGTCCGCAAGGCCTTCAAGAG  
CCACGTCTACGTCCAGTGCCAGGGGATCCCGCAGGGCTCCATCCTCTCCACGCTGCTCT  
GCAGCTGTGCTACGGCGACATGGAGAACAAGCTGTTTTCGGGGATTTCGGCGGGACGGGC  
TGCTCCTGCGTTTGGTGGATGATTTCTTGTGGTGACACCTCACCTCACCCAGCGAAAA  
CCTTCCTCAGGACCCTGGTCCGAGGTGTCCCTGAGTATGGCTGCGTGGTGAACCTGCGGA  
AGACAGTGGTGAACCTCCCTGTAGAAGACGAGGCCCTGGGTGGCAGCGCTTTTGTTCAGA  
TGCCGGCCCCAGGCCCTATTCCTTGGTGCGGCCCTGCTGCTGGATACCCGGACCCCTGGAGG  
TGACAGAGCGACTACTCCAGCTATGCCCGGACCTCCATCAGAGCCAGTCTCACCTTCAACC  
GCGGCTTCAAGGCTGGGAGGAACATGCGTCGCAAACTCTTTGGGGTCTTGGCGCTGAAGT  
GTCACAGCCTGTTTCTGGATTTGCAGGTGAACAGCCTCCAGACGGTGTGCACCAACATCT  
ACAAGATCCTCTGCTGCAGGCGTACAGGTTTCACGCATGTGTGCTGCAGCTCCCATTTC  
ATCAGCAAGTTTGAAGAACCCACATTTTCTGCGCGTCATCTCTGACACGGCCTCCC  
TCTGCTACTCCATCCTGAAAGCCAAGAACGCAGGGATGTGCTGGGGGCCAAGGGCGCCG  
CCGGCC7TCTGCCCTCCGAGGCCGTGAGTGGCTGTGCCACCAAGCATTCCTGCTCAAGC  
TGACTCGACACCGTGTACCTACGTGCCACTCCTGGGGTCACTCAGGACAGCCAGACGC  
AGCTGAGTCGGAAGCTCCCGGGGACGACGCTGACTGCCCTGGAGGCCGACGCCAACCCGG  
CACTGCCCTCAGACTTCAAGACCATCCTGGACTGATGGCCACCCGCCACAGCCAGGCCG  
AGAGCAGACACCAGCAGCCCTGTACGCCCGGGCTTACGTCCCAGGGAGGGAGGGCGGC  
CCACACCCAGGCCGTGACCCGTGGGAGTCTGAGGCCTGAGTGTGTTGGCCGAGGCCCT  
GCATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGCCTGAGCGAGTGTCCAGCCAAGGGC  
TGAGTGTCCAGCACACCTGCCGTCTTCACTTCCCCACAGGCTGGCGCTCGGCTCCACCCC  
AGGGCCAGCTTTTCTCACCAGGAGCCCGGCTTCCACTCCCCACATAGGAATAGTCCATC  
CCGAGTGGAGACCCCTGAGAAGGACCCTGGGAGCTCTGGGAATTTGGAGTGACCAAAGGTGT  
GCCCTGTACACAGGCGAGGACCCTGCACCTGGATGGGGGTCCCTGTGGGTCAAATTGGGG  
GGAGGTGCTGTGGGAGTAAATACTGAATATATGAGTTTTTCAGTTTTTG0AAAAA  
AAAAAAAAAAAAA

FIG. 18



23/103

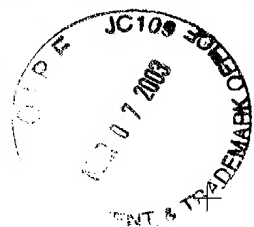
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 TyrValThrGluThrThrPheGlnLysAsnArgLeuPhe  
 PheTyrArgLysSerValTrpSerLysLeuGlnSerIle  
 GlyIleArgGlnHisLeuLysArgValGlnLeuArgGlu  
 LeuSerGluAlaGluValArgGlnHisArgGluAlaArg  
 ProAlaLeuLeuThrSerArgLeuArgPheIleProLys  
 ProAspGlyLeuArgProIleValAsnMetAspTyrVal  
 ValGlyAlaArgThrPheArgArgGluLysArgAlaGlu  
 ArgLeuThrSerArgValLysAlaLeuPheSerValLeu  
 AsnTyrGluArgAlaArgArgProGlyLeuLeuGlyAla  
 SerValLeuGlyLeuAspAspIleHisArgAlaTrpArg  
 ThrPheValLeuArgValArgAlaGlnAspProProPro  
 GluLeuTyrPheValLysValAspValThrGlyAlaTyr  
 AspThrIleProGlnAspArgLeuThrGluValIleAla  
 SerIleIleLysProGlnAsnThrTyrCysValArgArg  
 TyrAlaValValGlnLysAlaAlaHisGlyHisValArg  
 LysAlaPheLysSerHisValLeuArgProValProGly  
 AspProAlaGlyLeuHisProLeuHisAlaAlaLeuGln  
 ProValLeuArgArgHisGlyGluGlnAlaValCysGly  
 AspSerAlaGlyArgAlaAlaProAlaPheGlyGly

FIG. 19

															1
															met
GCAGCGCTGCGTCCTGCTGCGCACGTGGGAAGCCCTGGCCCCGGCCACCCCCGCG															ATG
															10
pro	arg	ala	pro	arg	cys	arg	ala	val	arg	ser	leu	leu	arg	ser	
CCG	CGC	GCT	CCC	CGC	TGC	CGA	GCC	GTG	CGC	TCC	CTG	CTG	CGC	AGC	
															20
his	tyr	arg	glu	val	leu	pro	leu	ala	thr	phe	val	arg	arg	leu	
CAC	TAC	CGC	GAG	GTG	CTG	CCG	CTG	GCC	ACG	TTC	GTG	CGG	CGC	CTG	
															30
															40
gly	pro	gln	gly	trp	arg	leu	val	gln	arg	gly	asp	pro	ala	ala	
GGG	CCC	CAG	GGC	TGG	CGG	CTG	GTG	CAG	CGC	GGG	GAC	CCG	GCG	GCT	
															50
phe	arg	ala	leu	val	ala	gln	cys	leu	val	cys	val	pro	trp	asp	
TTC	CGC	GCG	CTG	GTG	GCC	CAG	TGC	CTG	GTG	TGC	GTG	CCC	TGG	GAC	
															60
															70
ala	arg	pro	pro	pro	ala	ala	pro	ser	phe	arg	gln	val	ser	cys	
GCA	CGG	CCG	CCC	CCC	GCC	GCC	CCC	TCC	TTC	CGC	CAG	GTG	TCC	TGC	
															80
leu	lys	glu	leu	val	ala	arg	val	leu	gln	arg	leu	cys	glu	arg	
CTG	AAG	GAG	CTG	GTG	GCC	CGA	GTG	CTG	CAG	AGG	CTG	TGC	GAG	CGC	
															90
															100
gly	ala	lys	asn	val	leu	ala	phe	gly	phe	ala	leu	leu	asp	gly	
GGC	GCG	AAG	AAC	GTG	CTG	GCC	TTC	GGC	TTC	GCG	CTG	CTG	GAC	GGG	
															110
ala	arg	gly	gly	pro	pro	glu	ala	phe	thr	thr	ser	val	arg	ser	
GCC	CGC	GGG	GGC	CCC	CCC	GAG	GCC	TTC	ACC	ACC	AGC	GTG	CGC	AGC	
															120

FIG. 20

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24/103

130  
tyr leu pro asn thr val thr asp ala leu arg gly ser gly ala  
TAC CTG CCC AAC ACG GTG ACC GAC GCA CTG CGG GGG AGC GGG GCG

140  
trp gly leu leu leu arg arg val gly asp asp val leu val his  
TGG GGG CTG CTG CTG CGC CGC GTG GGC GAC GAC GTG CTG GTT CAC

150  
leu leu ala arg cys ala leu phe val leu val ala pro ser cys  
CTG CTG GCA CGC TGC GCG CTC TTT GTG CTG GTG GCT CCC AGC TGC

160  
ala tyr gln val cys gly pro pro leu tyr gln leu gly ala ala  
GCC TAC CAG GTG TGC GGG CCG CCG CTG TAC CAG CTC GGC GCT GCC

170  
thr gln ala arg pro pro pro his ala ser gly pro arg arg arg  
ACT CAG GCC CGG CCC CCG CCA CAC GCT AGT GGA CCC CGA AGG CGT

180  
leu gly cys glu arg ala trp asn his ser val arg glu ala gly  
CTG GGA TGC GAA CGG GCC TGG AAC CAT AGC GTC AGG GAG GCC GGG

190  
val pro leu gly leu pro ala pro gly ala arg arg arg gly gly  
GTC CCC CTG GGC CTG CCA GCC CCG GGT GCG AGG AGG CGC GGG GGC

200  
ser ala ser arg ser leu pro leu pro lys arg pro arg arg gly  
AGT GCC AGC CGA AGT CTG CCG TTG CCC AAG AGG CCC AGG CGT GGC

210  
ala ala pro glu pro glu arg thr pro val gly gln gly ser trp  
GCT GCC CCT GAG CCG GAG CGG ACG CCC GTT GGG CAG GGG TCC TGG

220  
ala his pro gly arg thr arg gly pro ser asp arg gly phe cys  
GCC CAC CCG GGC AGG ACG CGT GGA CCG AGT GAC CGT GGT TTC TGT

230  
val val ser pro ala arg pro ala glu glu ala thr ser leu glu  
GTG GTG TCA CCT GCC AGA CCC GCC GAA GAA GCC ACC TCT TTG GAG

240  
gly ala leu ser gly thr arg his ser his pro ser val gly arg  
GGT GCG CTC TCT GGC ACG CGC CAC TCC CAC CCA TCC GTG GGC CGC

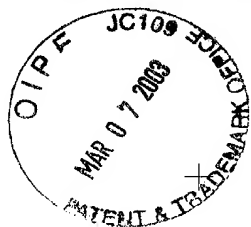
250  
gln his his ala gly pro pro ser thr ser arg pro pro arg pro  
CAG CAC CAC GCG GGC CCC CCA TCC ACA TCG CGG CCA CCA CGT CCC

260  
trp asp thr pro cys pro pro val tyr ala glu thr lys his phe  
TGG GAC ACG CCT TGT CCC CCG GTG TAC GCC GAG ACC AAG CAC TTC

270  
330

FIG. 20  
(CONTINUED)

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25/103

340  
leu tyr ser ser gly asp lys glu gln leu arg pro ser phe leu  
CTC TAC TCC TCA GGC GAC AAG GAG CAG CTG CGG CCC TCC TTC CTA

350  
leu ser ser leu arg pro ser leu thr gly ala arg arg leu val  
CTC AGC TCT CTG AGG CCC AGC CTG ACT GGC GCT CGG AGG CTC GTG

370  
glu thr ile phe leu gly ser arg pro trp met pro gly thr pro  
GAG ACC ATC TTT CTG GGT TCC AGG CCC TGG ATG CCA GGG ACT CCC

380  
arg arg leu pro arg leu pro gln arg tyr trp gln met arg pro  
CGC AGG TTG CCC CGC CTG CCC CAG CGC TAC TGG CAA ATG CGG CCC

390  
arg arg leu pro arg leu pro gln arg tyr trp gln met arg pro  
CGC AGG TTG CCC CGC CTG CCC CAG CGC TAC TGG CAA ATG CGG CCC

400  
leu phe leu glu leu leu gly asn his ala gln cys pro tyr gly  
CTG TTT CTG GAG CTG CTT GGG AAC CAC GCG CAG TGC CCC TAC GGG

410  
val leu leu lys thr his cys pro leu arg ala ala val thr pro  
GTG CTC CTC AAG ACG CAC TGC CCG CTG CGA GCT GCG GTC ACC CCA

430  
ala ala gly val cys ala arg glu lys pro gln gly ser val ala  
GCA GCC GGT GTC TGT GCC CGG GAG AAG CCC CAG GGC TCT GTG GCG

440  
ala pro glu glu glu asp thr asp pro arg arg leu val gln leu  
GCC CCC GAG GAG GAG GAC ACA GAC CCC CGT CGC CTG GTG CAG CTG

450  
ala pro glu glu glu asp thr asp pro arg arg leu val gln leu  
GCC CCC GAG GAG GAG GAC ACA GAC CCC CGT CGC CTG GTG CAG CTG

460  
leu arg gln his ser ser pro trp gln val tyr gly phe val arg  
CTC CGC CAG CAC AGC AGC CCC TGG CAG GTG TAC GGC TTC GTG CGG

470  
ala cys leu arg arg leu val pro pro gly leu trp gly ser arg  
GCC TGC CTG CGC CGG CTG GTG CCC CCA GGC CTC TGG GGC TCC AGG

480  
ala cys leu arg arg leu val pro pro gly leu trp gly ser arg  
GCC TGC CTG CGC CGG CTG GTG CCC CCA GGC CTC TGG GGC TCC AGG

490  
his asn glu arg arg phe leu arg asn thr lys lys phe ile ser  
CAC AAC GAA CGC CGC TTC CTC AGG AAC ACC AAG AAG TTC ATC TCC

500  
leu gly lys his ala lys leu ser leu gln glu leu thr trp lys  
CTG GGG AAG CAT GCC AAG CTC TCG CTG CAG GAG CTG ACG TGG AAG

510  
leu gly lys his ala lys leu ser leu gln glu leu thr trp lys  
CTG GGG AAG CAT GCC AAG CTC TCG CTG CAG GAG CTG ACG TGG AAG

520  
met ser val arg asp cys ala trp leu arg arg ser pro gly val  
ATG AGC GTG CGG GAC TGC GCT TGG CTG CGC AGG AGC CCA GGG GTT

530  
gly cys val pro ala ala glu his arg leu arg glu glu ile leu  
GGC TGT GTT CCG GCC GCA GAG CAC CGT CTG CGT GAG GAG ATC CTG

540  
gly cys val pro ala ala glu his arg leu arg glu glu ile leu  
GGC TGT GTT CCG GCC GCA GAG CAC CGT CTG CGT GAG GAG ATC CTG

FIG. 20  
(CONTINUED)

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26/103

550  
ala lys phe leu his trp leu met ser val tyr val val glu leu  
GCC AAG TTC CTG CAC TGG CTG ATG AGT GTG TAC GTC GTC GAG CTG

560  
leu arg ser phe phe tyr val thr glu thr thr phe gln lys asn  
CTC AGG TCT TTC TTT TAT GTC ACG GAG ACC ACG TTT CAA AAG AAC

570  
arg leu phe phe tyr arg lys ser val trp ser lys leu gln ser  
AGG CTC TTT TTC TAC CGG AAG AGT GTC TGG AGC AAG TTG CAA AGC

580  
ile gly ile arg gln his leu lys arg val gln leu arg glu leu  
ATT GGA ATC AGA CAG CAC TTG AAG AGG GTG CAG CTG CGG GAG CTG

590  
ser glu ala glu val arg gln his arg glu ala arg pro ala leu  
TCG GAA GCA GAG GTC AGG CAG CAT CGG GAA GCC AGG CCC GCC CTG

600  
leu thr ser arg leu arg phe ile pro lys pro asp gly leu arg  
CTG ACG TCC AGA CTC CGC TTC ATC CCC AAG CCT GAC GGG CTG CGG

610  
pro ile val asn met asp tyr val val gly ala arg thr phe arg  
CCG ATT GTG AAC ATG GAC TAC GTC GTG GGA GCC AGA ACG TTC CGC

620  
arg glu lys arg ala glu arg leu thr ser arg val lys ala leu  
AGA GAA AAG AGG GCC GAG CGT CTC ACC TCG AGG GTG AAG GCA CTG

630  
phe ser val leu asn tyr glu arg ala arg arg pro gly leu leu  
TTC AGC GTG CTC AAC TAC GAG CGG GCG CGG CGC CCC GGC CTC CTG

640  
gly ala ser val leu gly leu asp asp ile his arg ala trp arg  
GGC GCC TCT GTG CTG GGC CTG GAC GAT ATC CAC AGG GCC TGG CGC

650  
thr phe val leu arg val arg ala gln asp pro pro pro glu leu  
ACC TTC GTG CTG CGT GTG CGG GCC CAG GAC CCG CCG CCT GAG CTG

660  
tyr phe val lys val asp val thr gly ala tyr asp thr ile pro  
TAC TTT GTC AAG GTG GAT GTG ACG GGC GCG TAC GAC ACC ATC CCC

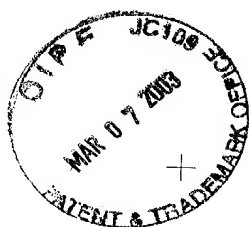
670  
gln asp arg leu thr glu val ile ala ser ile ile lys pro gln  
CAG GAC AGG CTC ACG GAG GTC ATC GCC AGC ATC ATC AAA CCC CAG

680  
asn thr tyr cys val arg arg tyr ala val val gln lys ala ala  
AAC ACG TAC TGC GTG CGT CGG TAT GCC GTG GTC CAG AAG GCC GCC

690  
700  
710  
720  
730  
740  
750

FIG. 20  
(CONTINUED)

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27/103

his gly his val arg lys ala phe 760 ser his val leu arg pro  
CAT GGG CAC GTC CGC AAG GCC TTC AAG AGC CAC GTC CTA CGT CCA

770 780  
val pro gly asp pro ala gly leu his pro leu his ala ala leu  
GTG CCA GGG GAT CCC GCA GGG CTC CAT CCT CTC CAC GCT GCT CTG

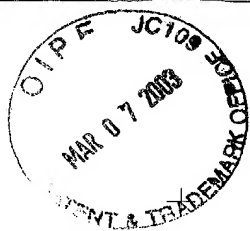
790  
gln pro val leu arg arg his gly glu gln ala val cys gly asp  
CAG CCT GTG CTA CGG CGA CAT GGA GAA CAA GCT GTT TGC GGG GAT

800 807  
ser ala gly arg ala ala pro ala phe gly gly OP  
TCG GCG GGA CGG GCT GCT CCT GCG TTT GGT GGA TGA TTTCTTGTGGT

GACACCTCACCTCACCCACGCGAAAACCTTCCTCAGGACCCTGGTCCGAGGTGTCCCTGA  
GTATGGCTGCGTGGTGAACCTGCGGAAGACAGTGGTGAACCTTCCCTGTAGAAGACGAGGC  
CCTGGGTGGCACGGCTTTTGTTCAGATGCCGGCCACGGCCTATTCCCCTGGTGC GGCCCT  
GCTGCTGGATACCCGACCCCTGGAGGTGCAGAGCGACTACTCCAGCTATGCCCGGACCTC  
CATCAGAGCCAGTCTCACCTTCAACCGCGGCTTCAAGGCTGGGAGGAACATGCGTCGCAA  
ACTCTTTGGGGTCTTGCGGCTGAAGTGTACAGCCTGTTTCTGGATTGTCAGGTGAACAG  
CCTCCAGACGGTGTGCACCAACATCTACAAGATCCTCCTGCTGCAGGCGTACAGGTTTCA  
CGCATGTGTGCTGCAGCTCCCATTTTCATCAGCAAGTTTGGAAGAACCCACATTTTTCT  
GCGCGTCATCTCTGACACGGCCTCCCTCTGCTACTCCATCCTGAAAGCCAAGAACGCAGG  
GATGTGCTGCGTGGGGGCCAAGGGCGCCGCGGCCCTCTGCCCTCCGAGGCCGTGCAGTGGCT  
GTGCCACCAAGCATTCCTGCTCAAGCTGACTCGACACCGTGTACCTACGTGCCACTCCT  
GGGGTCACTCAGGACAGCCAGACGCAGCTGAGTCGGAAGCTCCCGGGGACGACGCTGAC  
TGCCCTGGAGGCCGAGCCAACCCGGCACTGCCCTCAGACTTCAAGACCATCCTGGACTG  
ATGGCCACCCGCCACAGCCAGGCCGAGAGCAGACACCAGCAGCCCTGTACAGCCGGGCT  
CTACGTCCCAGGGAGGGAGGGGCGGCCACACCCAGGCCCGCACCGCTGGGAGTCTGAGG  
CCTGAGTGAGTGTTTGGCCGAGGCCTGCATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAG  
GCCTGAGCGAGTGTCCAGCCAAGGGCTGAGTGTCCAGCACACCTGCCGTCTTCACTTCCC  
CACAGGCTGGCGCTCGGCTCCACCCAGGGCCAGCTTTTCTCACCAGGAGCCCGGCTTC  
CACTCCCCACATAGGAATAGTCCATCCCCAGATTGCCATTGTTACCCCTCGCCCTGCC  
CTCCTTTGCCTTCCACCCCAACCATCCAGGTGGAGACCCTGAGAAGGACCCTGGGAGCTC  
TGGAATTTGGAGTGACCAAAGGTGTGCCCTGTACACAGGCGAGGACCCTGCACCTGGAT  
GGGGTCCCTGTGGGTCAAATTGGGGGGAGGTGCTGTGGGAGTAAATACTGAATATATG  
AGTTTTTCAGTTTTTGA

FIG. 20  
(CONTINUED)

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28/103

1 CCATGGGACCCACTGCAGGGGCAGCTGGGAGGCTGCAGGCTTCAGGTCCCAGTGGGGTTG  
GGTACCCTGGGTGACGTCCCCGTCGACCCTCCGACGTCCGAAGTCCAGGGTCACCCCAAC

61 CCATCTGCCAGTAGAAACCTGATGTAGAATCAGGGCGCGAGTGTGGACACTGTCCTGAAT  
GGTAGACGGTCATCTTTGGACTACATCTTAGTCCCGCGCTCACACCTGTGACAGGACTTA

121 CTCAATGTCTCAGTGTGTGCTGAAACATGTAGAAATTAAAGTCCATCCCTCCTACTCTAC  
GAGTTACAGAGTCACACACGACTTTGTACATCTTTAATTTTCAGGTAGGGAGGATGAGATG

181 TGGGATTGAGCCCCCTTCCCTATCCCCCCCCAGGGGCAGAGGAGTTCTCTCACTCCTGTG  
ACCCTAACTCGGGGAAGGGATAGGGGGGGGTCCCGTCTCCTCAAGGAGAGTGAGGACAC

241 GAGGAAGGAATGATACTTTGTTATTTTTCAGTGTGTTACTGAATCCACTGTTTCATTTG  
CTCCTTCCTTACTATGAAACAATAAAAAGTGACGACCATGACTTAGGTGACAAAGTAAAC

\*\*\*\*\*

301 TTGGTTTGTGTTTGTGTTTGTGTTTGTGAGAGGCGGTTTCACTCTTGTTGCTCAGGCTGGAGGGAG  
AACCAAACAAACAAACAAACAACTCTCCGCCAAAGTGAGAACAACGAGTCCGACCTCCCTC

\*\*\*\*\*

361 TGCAATGGCGCGATCTTGGCTTACTGCAGCCTCTGCCTCCAGGTTCAAGTGATTCTCCT  
ACGTTACCGCGCTAGAACCGAATGACGTCGGAGACGGAGGGTCCAAGTTCACTAAGAGGA

\*\*\*\*\*

421 GCTTCCGCCTCCCATTTGGCTGGGATTACAGGCACCCGCCACCATGCCCAGCTAATTTTT  
CGAAGGCGGAGGGTAAACCGACCTAATGTCCGTGGGCGGTGGTACGGGTTCGATTAAAAA

\*\*\*\*\*

481 TGTATTTTTAGTAGAGACGGGGGTGGGGGTGGGGTTCACCATGTTGGCCAGGCTGGTCTC  
ACATAAAAATCATCTCTGCCCCACCCCCACCCCAAGTGGTACAACCGGTCCGACCAGAG

\*\*\*\*\*

541 GAACCTCTGACCTCAGATGATCCACCTGCCTCTGCCTCCTAAAGTGCTGGGATTACAGGT  
CTTGAAGACTGGAGTCTACTAGGTGGACGGAGACGGAGGATTTACGACCCCTAATGTCCA

\*\*\*\*\*

601 GTGAGCCACCATGCCCAGCTCAGAATTTACTCTGTTTAGAAACATCTGGGTCTGAGGTAG  
CACTCGGTGGTACGGGTGAGTCTTAAATGAGACAAATCTTTGTAGACCCAGACTCCATC

\*\*\*\*\*

661 GAAGCTCACCCCACTCAAGTGTGTGGTGTGTTTAAAGCCAATGATAGAATTTTTTTATTGT  
CTTCGAGTGGGGTGAGTTCACAACACCACAAAATTCGGTTACTATCTTAAAAAATAACA

721 TGTTAGAACACTCTTGATGTTTTTACACTGTGATGACTAAGACATCATCAGCTTTTCAAAG  
ACAATCTTGTGAGAACTACAAAATGTGACACTACTGATTCTGTAGTAGTCGAAAAGTTTC

FIG. 21

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29/103

CAP

\*\*\*\*\*>

781 ACACACTAACTGCACCCATAATACTGGGGTGTCTTCTGGGTATCAGCGATCTTCATTGAA  
TGTGTGATTGACGTGGGTATTATGACCCACAGAAGACCCATAGTCGCTAGAAGTAACTT

CAP

\*\*\*\*\*

841 TGCCGGGAGGCGTTTCTCGCCATGCACATGGTGTAAATTACTCCAGCATAATCTTCTGC  
ACGGCCCTCCGCAAAGGAGCGGTACGTGTACCACAATTAATGAGGTCGTATTAGAAGACG

\*\*\*>

901 TTCCATTTCTTCTCTTCCCTCTTTTAAAATTGTGTTTTCTATGTTGGCTTCTCTGCAGAG  
AAGGTAAAGAAGAGAAGGGAGAAAATTTTAAACACAAAAGATACAACCGAAGAGACGTCTC

CAP

\*\*\*\*\*>

961 AACCAGTGTAAGCTACAACCTTAACCTTTTGTGGAAACAAATTTTCAAACCGCCCCCTTTGC  
TTGGTCACATTCGATGTTGAATTGAAAACAACCTTGTTTAAAAGGTTTGGCGGGGAAACG

1021 CCTAGTGGCAGAGACAATTCACAAACACAGCCCTTTAAAAGGCTTAGGGATCACTAAGG  
GGATCACCGTCTCTGTAAAGTGTGTGTGTCGGGAAATTTTCCGAATCCCTAGTGATTCC

1081 GGATTTCTAGAAGAGCGACCCGTAATCCTTAAGTATTTACAAGACGAGGCTAACCTCCAG  
CCTAAAGATCTTCTCGCTGGGCATTAGGAATTCATAAATGTTCTGCTCCGATTGGAGGTC

1141 CGAGCGTGACAGCCCAGGGAGGGTGCAGGCGCTGTTCAAATGCTAAGCTTCCATAAATAA  
GCTCGCACTGTCCGGTCCCTCCCACGCTCCGGACAAGTTTACGATTCTGAAGGTATTTATT

1201 AGCAAATTTCTCCGGCAGTTTCTGGAAAGTAGGAAAGGTTAACATTTAAGGTTGCGTTT  
TCGTTTAAAGGAGGCCGTCAAAGACCTTTTCATCCTTTCCAATTGTAAATTCACGCAAA

1261 GTTAGCATTTTCAGTGTGTTGCCGACCTCAGCTAACAGCATCCCTGCAAGGCCTCGGGAGAC  
CAATCGTAAAGTCACAAACGGCTGGAGTCGATTGTCTGCTAGGGACGTTCCGGAGCCCTCTG

1321 CCAGAAAGTTTCTCGCCCCCTTAGATCCAAACTTGAGCAACCCGGAGTCTGGATTCTTGGA  
GGTCTTCAAAGAGCGGGGAATCTAGGTTTGAACCTGTTGGGCCTCAGACCTAAGGACCCT

TopoII

\*\*\*\*\*>

1381 AGTCCTCAGCTGTCCTGCGGTTGTGCCGGGGCCCCAGGTCTGGAGGGGACCAGTGGCCGT  
TCAGGAGTCGACAGGACGCCAACACGGCCCCGGGTCCAGACCTCCCCTGGTCACCGGCA

1441 GTGGCTTCTACTGCTGGGCTGGAAGTCGGGCCTCCTAGCTCTGCAGTCCGAGGCTTGAG  
CACCGAAGATGACGACCCGACCTTCAGCCCCGAGGATCGAGACGTGAGGCTCCGAACCTC

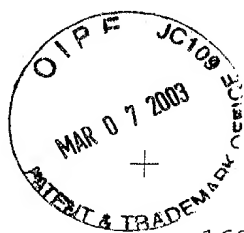
1501 CCAGGTGCCTGGACCCCGAGGCTGCCCTCCACCCTGTGCGGGCGGGATGTGACCAGATGT  
GGTCCACGGACCTGGGGCTCCGACGGGAGGTGGGACACGCCCGCCCTACACTGGTCTACA

1561 TGGCCTCATCTGCCAGACAGAGTGCCGGGGCCCCAGGGTCAAGGCCGTTGTGGCTGGTGTG  
ACCGGAGTAGACGGTCTGTCTCACGGCCCCGGGTCCAGTTCCGGCAACACCGACCACAC

1621 AGGCGCCCGGTGCGCGGCCAGCAGGAGCGCCTGGCTCCATTTCCACCCCTTTCTCGACGG  
TCCGCGGGCCACGCGCCGGTCTGCTCTGCGGACCGAGGTAAAGGGTGGGAAAGAGCTGCC

FIG. 21  
(CONTINUED)

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30/103

1681 GACCGCCCCGGTGGGTGATTAACAGATATTGGGGTGGTTTGCTCATGGTGGGGACCCCTT  
CTGGCGGGGCCACCCACTAATTGTCTATAACCCACCAAACGAGTACCACCCCTGGGGAA  
1741 CGCCGCCTGAGAACCTGCAAAGAGAAAATGACGGGCCTGTGTCAAGGAGCCCAAGTCGCGG  
GCGGCGGACTCTTGGACGTTTCTCTTTACTGCCCGGACACAGTTCTCTCGGGTTCAGCGCC  
1801 GGAAGTGTTCAGGGAGGCACTCCGGGAGGTCCCGCGTGCCCGTCCAGGGAGCAATGCGT  
CCTTCACAACGTCCCTCCGTGAGGCCCTCCAGGGCGCACGGGCAGGTCCCTCGTTACGCA  
1861 CCTCGGGTTCGTCCCCAGCCGCGTCTACGCGCCTCCGTCTCCCTTCACGTCCGGCATT  
GGAGCCCAAGCAGGGGTCCGGCGCAGATGCGCGGAGGCAGGAGGGGAAGTCAGGCCGTAA  
1921 CGTGGTGGCCGAGCCCCGACGCCCCGCGTCCGGACCTGGAGGCAGCCCTGGGTCTCCGGA  
GCACCACGGGCCTCGGGCTGCGGGGCGCAGGCCTGGACCTCCGTGCGGACCCAGAGGCCT  
1981 TCAGGCCAGCGGCCAAAGGGTTCGCGCACGACCTGTTCCAGGGCCTCCACATCATGGC  
AGTCCGGTCGCGGTTTCCAGCGGCGTGCGTGACAAGGGTCCCGGAGGTGTAGTACCG  
2041 CCCTCCCTCGGGTTACCCACAGCCTAGGCCGATTGACCTCTCTCCGCTGGGGCCCTCG  
GGGAGGGAGCCCAATGGGGTGTGCGATCCGGCTAAGCTGGAGAGAGGCGACCCCGGGAGC

Sp1

\*\*\*\*\*

2101 CTGGCGTCCCTGCACCCTGGGAGCGCGAGCGGCGCGGGCGGGGAAGCGCGGCCAGAC  
GACCGCAGGGACGTGGGACCCTCGCGCTCGCCGCGCGCCCGCCCTTCGCGCCGGGTCTG  
2161 CCCCAGGTCCGCCCCGAGCAGCTGCGCTGTGCGGGCCAGGCCGGGTCCCAGTGGATTTCG  
GGGGCCAGGCGGGCCTCGTCGACGCGACAGCCCCGCTCCGGCCCCAGGGTACCTAAGC  
2221 CGGGCAACAGACGCCCAGGACCGCGCTTCCACGTGGCGGAGGGACTGGGGACCCGGGCA  
GCCCCGTTGTCTGCGGGTCTTGCGCGCAAGGGTGCACCGCCTCCCTGACCCCTGGGCCCGT

Sp1

=====

E2F

\*\*\*\*\*

2281 CCGGTCCTGCCCCCTTCACCTTCCAGCTCCGCCTCGTCCGCGCGGAACCCCGCCCCGTCCC  
GGCCAGGACGGGGAAGTGGAAGGTCGAGGCGGAGCAGGCGCGCCTTGGGGCGGGGACAGG  
2341 GAACCCCTTCCCGGGTCCCCGGCCCCAGCCCCCTCCGGGCCATCCCAGCCCGTCCCGTTCCCT  
CTTGGAAGGGCCCAGGGGCCGGGTGCGGGAAGGCCCGGTAGGGTCGGGCAGGGCAAGGA

Sp1

=====

E2F

\*\*\*\*\*

NFkB

\*\*\*\*\*

\*\*\*\*\*

2401 TTTCCGCGGCCCCGCCCTCTCCTCGCGGCGCGAGTTTCAGGCAGCGCTGCGTCTCTGCTGC  
AAAGGCGCCGGGGCGGGAGAGAGCGCCGCGCTCAAAGTCCGTGCGACGCAGGACGACG

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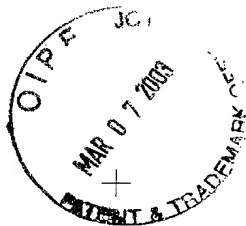
\*\*\*\*\*>

2461 GCACGTGGGAAGCCCTGGCCCCGGCCACCCCGCGATGCCGCGCGCTCCCCGCTGCCGAG  
CGTGACCCCTTCGGGACCGGGGCCGGTGGGGGCGCTACGGCGCGCGAGGGGCGACGGCTC

2521 CCGTGCGCTCCCTGCTGCGCAGCCACTACCGCGAGGTGCTGCCGCTGGCCACGTTTCGTGC  
GGCACGCGAGGGACGACGCTCGGTGATGGCGCTCCACGACGGCGACCGGTGCAAGCACG

FIG. 21  
(CONTINUED)

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31/103

E2F

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2581 GGCGCCTGGGGCCCCAGGGCTGGCGGCTGGTGCAGCGCGGGGACCCGGCGGCTTTCCGCG  
CCGCGGACCCCGGGTCCCCGACCGCCGACCACGTCGCGCCCCTGGGCCGCGGAAAGGCGC

\*

2641 CGCTGGTGGCCAGTGCCTGGTGTGCGTGCCTTGGGACGCACGGCCGCCCCCGCGCCC  
GCGACCACCGGGTCACGGACCACACGCACGGGACCCTGCGTGCCGGCGGGGGCGGCGGG

NFkB

=====

\*\*\*\*\*

2701 CCTCCTTCCGCCAGGTGGGCCTCCCCGGGGTCCGCGTCCGGCTGGGGTTGAGGGCGGCCG  
GGAGGAAGGCGGTCCACCCGAGGGGCCCCAGCCGAGGCCGACCCCACTCCCCCGCGC

Topo\_II\_cleavag

::::::::::::

NFkB

+++++++

NFkB

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Intron1

\*\*\*\*\*>

2761 GGGGGAACCAGCGACATGCGGAGAGCAGCGCAGGCGACTCAGGGCGCTTCCCCGCGAGGT  
CCCCCTTGGTCGCTGTACGCCTCTCGTCGCGTCCGCTGAGTCCCGCGAAGGGGGCGTCCA

e\_site

::::

2821 GTCCTGCCTGAAGGAGCTGGTGGCCCGAGTGCTGCAGAGGCTGTGCGAGCGGGCGCGAA  
CAGGACGGACTTCCTCGACCACCGGGCTCACGACGTCTCCGACACGCTCGCGCCGCGCTT

2881 GAACGTGCTGGCCTTCGGCTTCGCGCTGCTGGACGGGGCCCGGGGGCCCCCGAGGC  
CTTGACAGACCGGAAGCCGAAGCGGACGACCTGCCCCGGGCGCCCCGGGGGGGCTCCG

2941 CTTACCAACCAGCGTGCGCAGCTACCTGCCAACACGGTGACCGACGCACTGCGGGGGAG  
GAAGTGGTGGTTCGCACGCGTCGATGGACGGGTGTGCCACTGGCTGCGTGACGCCCCCTC

3001 CGGGGCGTGGGGGCTGCTGCTGCGCCGCGTGGGCGACGACGTGCTGGTTACCTGCTGGC  
GCCCCGACCCCCGACGACGACGCGGCGCACCCGCTGCTGCACGACCAAGTGACGACCG

3061 ACGCTGCGCGCTCTTTGTGCTGGTGGCTCCCAGCTGCGCCTACCAGGTGTGCGGGCCGCC  
TGCGACGCGCGAGAAACACGACCACCGAGGGTCGACGCGGATGGTCCACACGCCCGGCGG

3121 GCTGTACCAGCTCGGCGCTGCCACTCAGGCCCGGCCCGCCACACGCTAGTGGAACCCG  
CGACATGGTTCGAGCCGCGACGGTGAGTCCGGGCGGGGGCGGTGTGCGATCACCTGGGGC

3181 AAGGCGTCTGGGATGCGAACGGGCCTGGAACCATAGCGTCAGGGAGGCCGGGGTCCCCCT  
TTCCGCAGACCCTACGCTTGCCCGGACCTTGGTATCGCAGTCCCTCCGGCCCCAGGGGGA

3241 GGGCCTGCCAGCCCCGGGTGCGAGGAGGCGCGGGGGCAGTGCCAGCCGAAGTCTGCCGTT  
CCCGGACGGTCGGGGCCCACGCTCCTCCGCGCCCCCGTCACGGTCGGCTTCAGACGGCAA

3301 GCCCAAGAGGCCAGGCGTGGCGCTGCCCTGAGCCGGAGCGGACGCCCCGTTGGGCAGGG  
CGGGTTCTCCGGGTCCGCACCGCGACGGGGACTCGGCCTCGCCTGCGGGCAACCCGTCCC

FIG. 21  
(CONTINUED)

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32/103

3361 GTCCTGGGCCCCACCCGGGCAGGACGCGTGACCGTGACCGTGGTTTCTGTGTGGTGTC  
CAGGACCCGGGTGGGCCCCGTCTGCGCACCTGGCTCACTGGCACCAAAGACACACCACAG

3421 ACCTGCCAGACCCGCCGAAGAAGCCACCTCTTTGGAGGGTGCGCTCTCTGGCACGCGCCA  
TGGACGGTCTGGGCGGCTTCTTCGGTGGAGAAACCTCCACGCGAGAGACCGTGCGCGGT

3481 CTCCCACCCATCCGTGGGCGGCCAGCACACGCGGGCCCCCATCCACATCGCGGCCACC  
GAGGGTGGGTAGGCACCCGGCGGTCTGTGTGCGCCGGGGGGTAGGTGTAGCGCCGGTGG

3541 ACGTCCCTGGGACACGCCTTGTCCCCCGGTGTACGCCGAGACCAAGCACTTCTCTACTC  
TGCAGGGACCTGTGCGGAACAGGGGGCCACATGCGGCTCTGGTTCGTGAAGGAGATGAG

3601 CTCAGGCGACAAGGAGCAGCTGCGGCCCTCCTTCTACTCAGCTCTCTGAGGCCAGCCT  
GAGTCCGCTGTTCCTCGTCGACGCCGGGAGGAAGGATGAGTCGAGAGACTCCGGGTCCGA

3661 GACTGGCGCTCGGAGGCTCGTGGAGACCATCTTTCTGGGTTCAGGCCCTGGATGCCAGG  
CTGACCGCGAGCCTCCGAGCACCTCTGGTAGAAAGACCCAAGTCCGGGACCTACGGTCC

3721 GACTCCCCGCGAGGTTGCCCCGCTGCCCGAGCGCTACTGGCAAATGCGGGCCCCTGTTTCT  
CTGAGGGGCGTCCAACGGGGCGGACGGGGTTCGCGATGACCGTTTACGCCGGGGACAAAGA

3781 GGAGCTGCTTGGGAACCACGCGCAGTGCCCTACGGGGTGCTCCTCAAGACGCACTGCCC  
CCTCGACGAACCTTGGTGC GCGTACGGGGATGCCCCACGAGGAGTTCTGCGTGACGGG

3841 GCTGCGAGCTGCGGTCACCCCAGCAGCCGGTGTCTGTGCCCCGGGAGAAGCCCCAGGGCTC  
CGACGCTCGACGCCAGTGGGGTCTGTCGGCCACAGACACGGGCCCTCTTCGGGGTCCCGAG

3901 TGTGGCGGGCCCCGAGGAGGAGGACACAGACCCCGTTCGCTGGTGCAGCTGCTCCGCCA  
ACACCGCCGGGGGCTCCTCCTCCTGTGTCTGGGGGCGAGCGGACCACGTCGACGAGGCGGT

3961 GCACAGCAGCCCCTGGCAGGTGTACGGCTTCGTGCGGGCCTGCCTGCGCCGGCTGGTGCC  
CGTGTCTGTCGGGGACCGTCCACATGCCGAAGCACGCCCGGACGGACGCGGCCGACCACGG

4021 CCCAGGCCTCTGGGGCTCCAGGCACAACGAACGCCGCTTCTCAGGAACACCAAGAAGTT  
GGGTCCGGAGACCCCGAGGTCCGTGTTGCTTGC GGGCGAAGGAGTCTTGTGGTTCCTCAA

4081 CATCTCCCTGGGGAAGCATGCCAAGCTCTCGCTGCAGGAGCTGACGTGGAAGATGAGCGT  
GTAGAGGGACCCCTTCGTACGGTTCGAGAGCGACGTCTCTGACTGCACCTTCTACTCGCA

\*\*\*\*\*

4141 GCGGGACTGCGCTTGCGTGC GCGAGGAGCCAGGTGAGGAGGTGGTGGCCGTCGAGGGCCC  
CGCCCTGACGCGAACCAGCGCTCCTCGGGTCCACTCCTCCACCACCGCAGTCCCGGG

Intron2

\*\*\*\*\*

4201 AGGCCCCAGAGCTGAATGCAGTAGGGGCTCAGAAAAGGGGGCAGGCAGAGCCCTGGTCTT  
TCCGGGGTCTCGACTTACGTCATCCCCGAGTCTTTTCCCCCGTCCGTCTCGGGACCAGGA

\*\*\*\*\*

4261 CCTGTCTCCATCGTCACTGCGGACACGTGGCTTTTCGCTCAGGACGTGAGTGACACG  
GGACAGAGGTAGCAGTGCACCCGTGTGCACCGAAAAGCGAGTCTCTGAGCTCACCTGTGC

\*\*\*\*\*>

4321 GTGATCGAGGTTCGAC  
CACTAGCTCCAGCTG

FIG. 21  
(CONTINUED)

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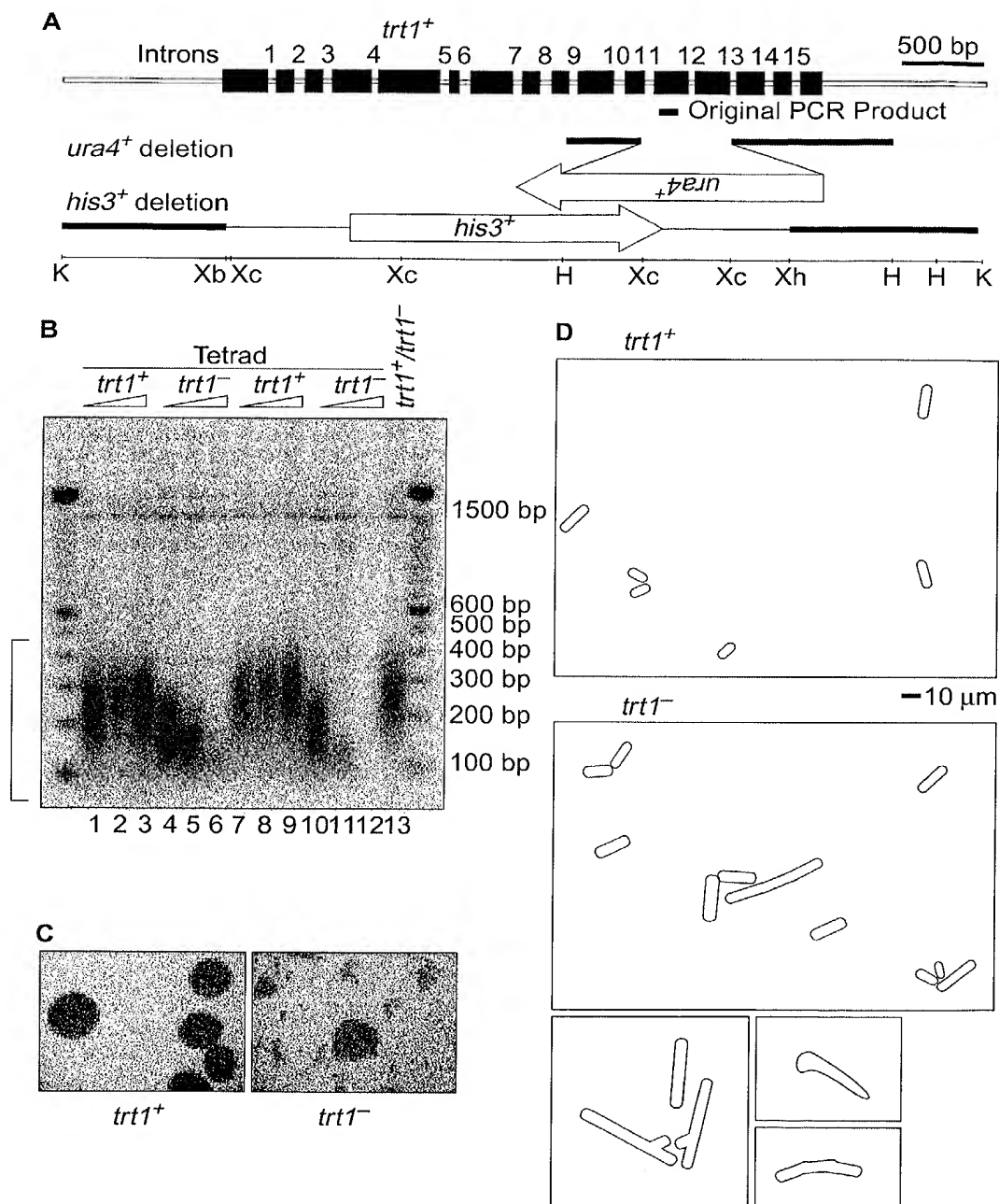


FIG. 22

34/103

gccaagtctcctgcactggctgatgagtgtgtacgtcgtcgagctgctcaggtctttttt  
tatgtcacggagaccacgtttcaaaagaacaggctctttttctaccggaagagtgtctgg  
agcaagtgcgaagcattggaatcagacagcacttgaagaggggtgcagctgcgggacgtg  
tcggaagcagaggtcaggcagcatcggaagccaggcccgccctgctgacgtccagactc  
cgcttcacccccaaagcctgacgggctgcggccgattgtgaacatggactacgtcgtggga  
gccagaacgttcgcagagaaaagagggccgagcgtctcacctcgaggggtgaaggcactg  
ttcagcgtgctcaactacgagcgggcccgcg

FIG. 23

TCTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTCGTGGCTCACCTGCAGGAG  
ACCAGCCCGCTGAGGGATGCCGTGCTCATCGAGCAGAGCTCCTCCCTGAATGAGGCC  
AGCAGTGGCCTCTTCGACGTCTTCTACGCTTCATGTGCCACCACGCCGTGCGCATC  
AGGGGCAAGTC

FIG. 24

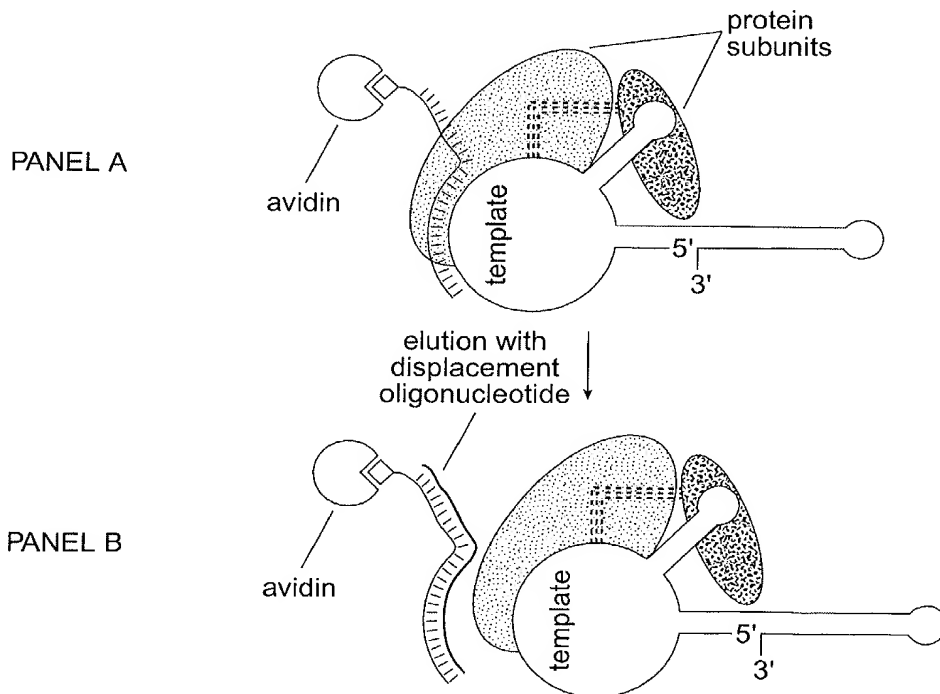
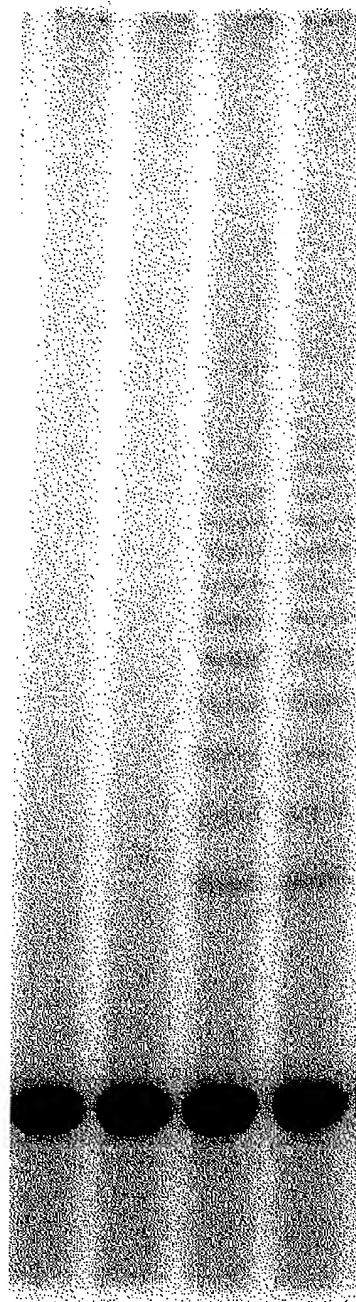


FIG. 26



35/103

pBB5212 pGRN133

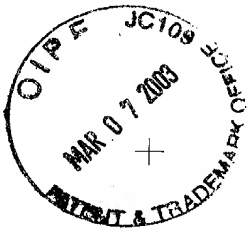


← Internal Control

Approximate Cell No. 5,000 5,000 5,000 5,000

*FIG. 25*

+



36/103

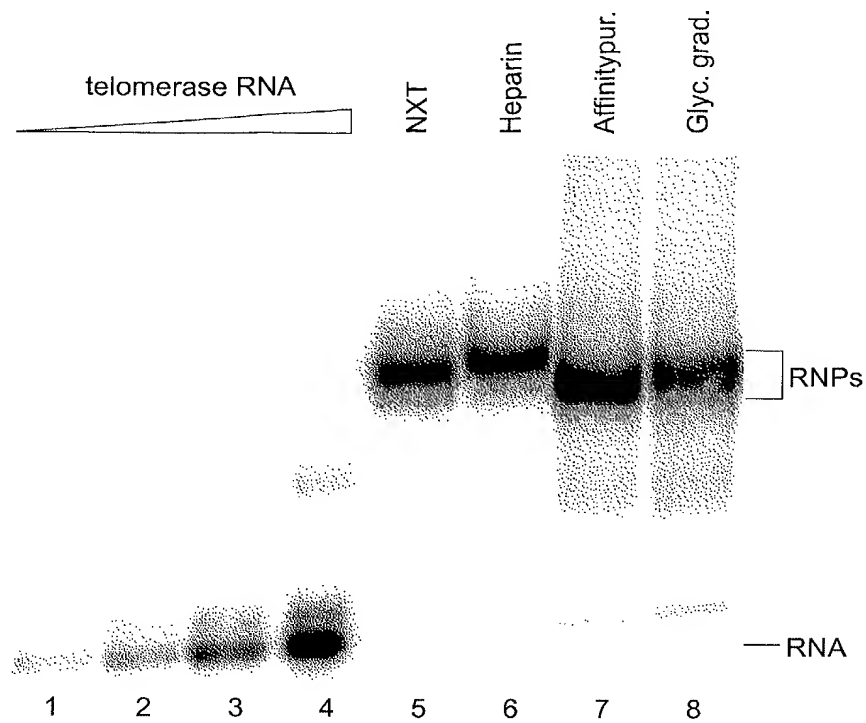


FIG. 27

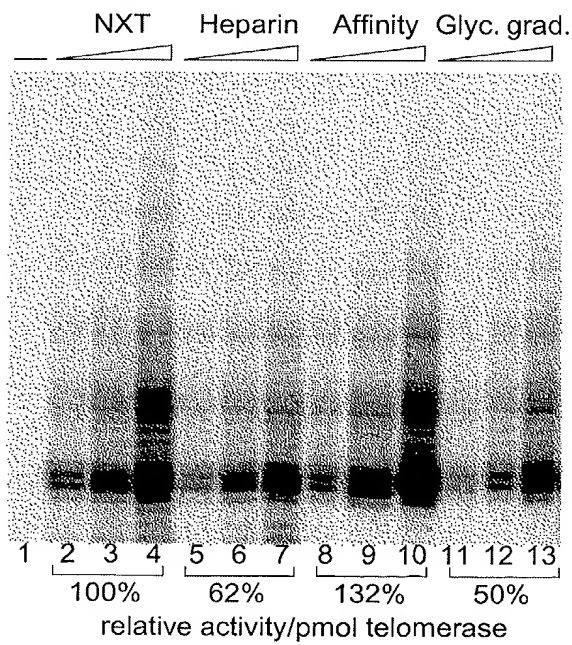
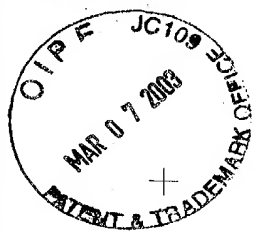


FIG. 28





37/103

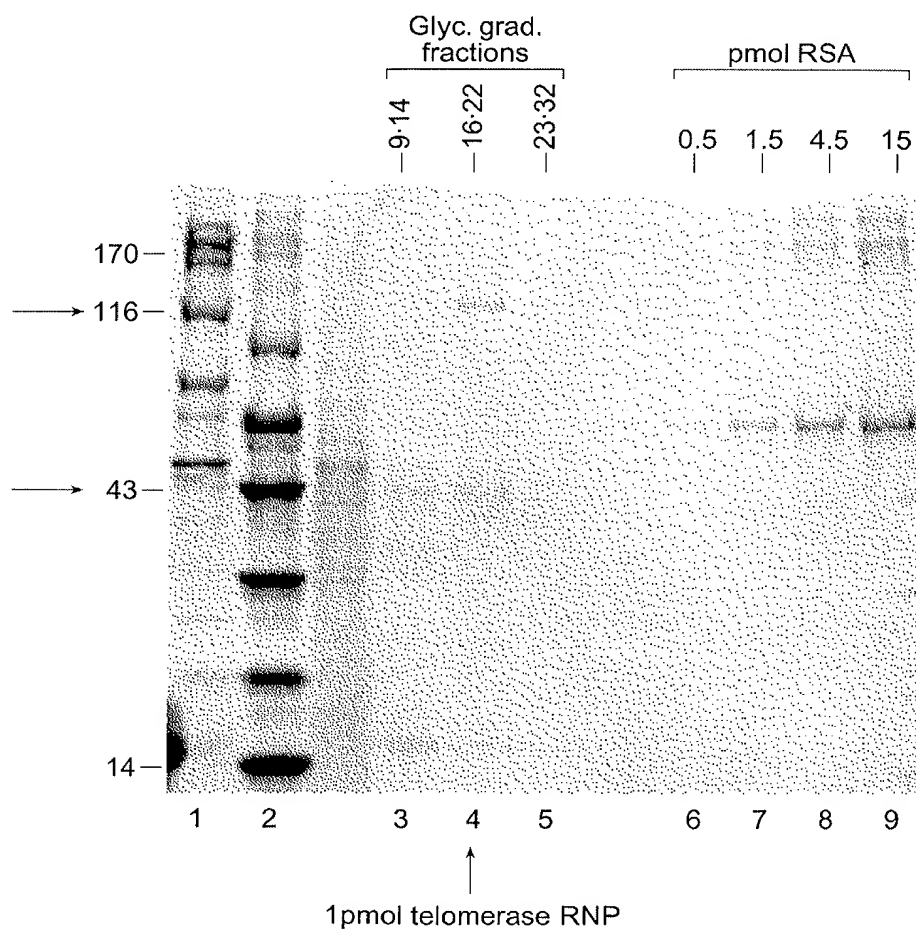
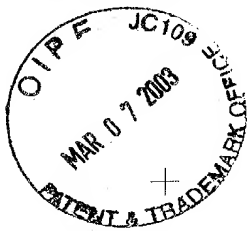


FIG. 29



38/103

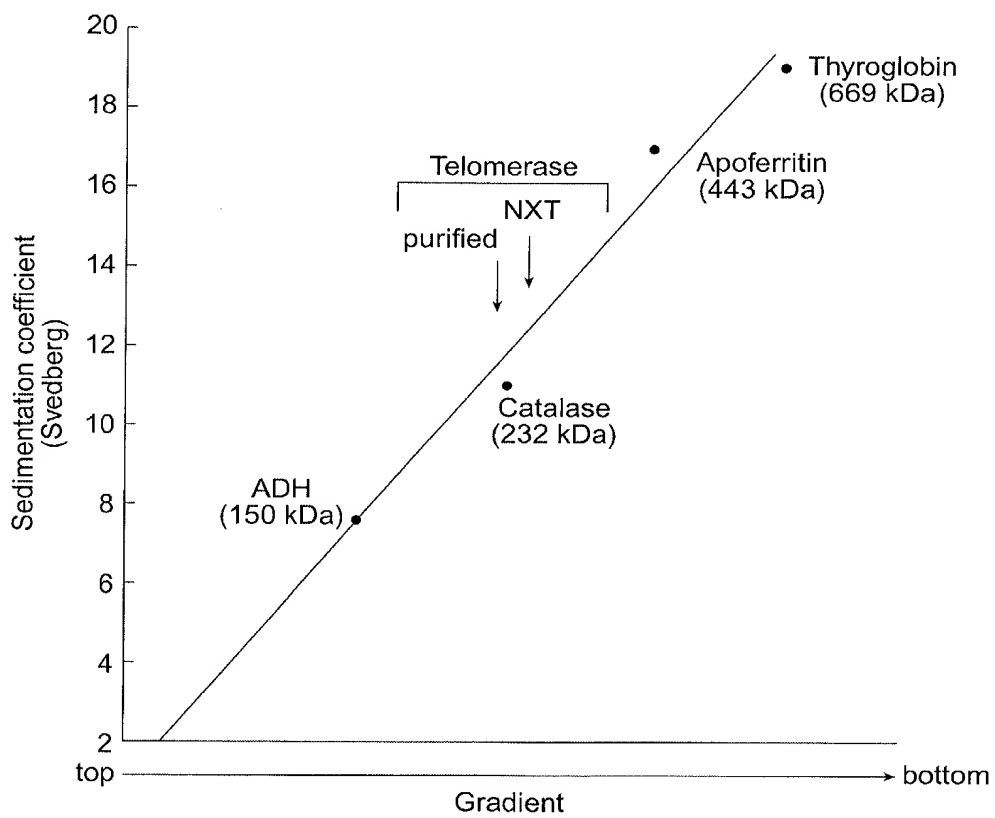


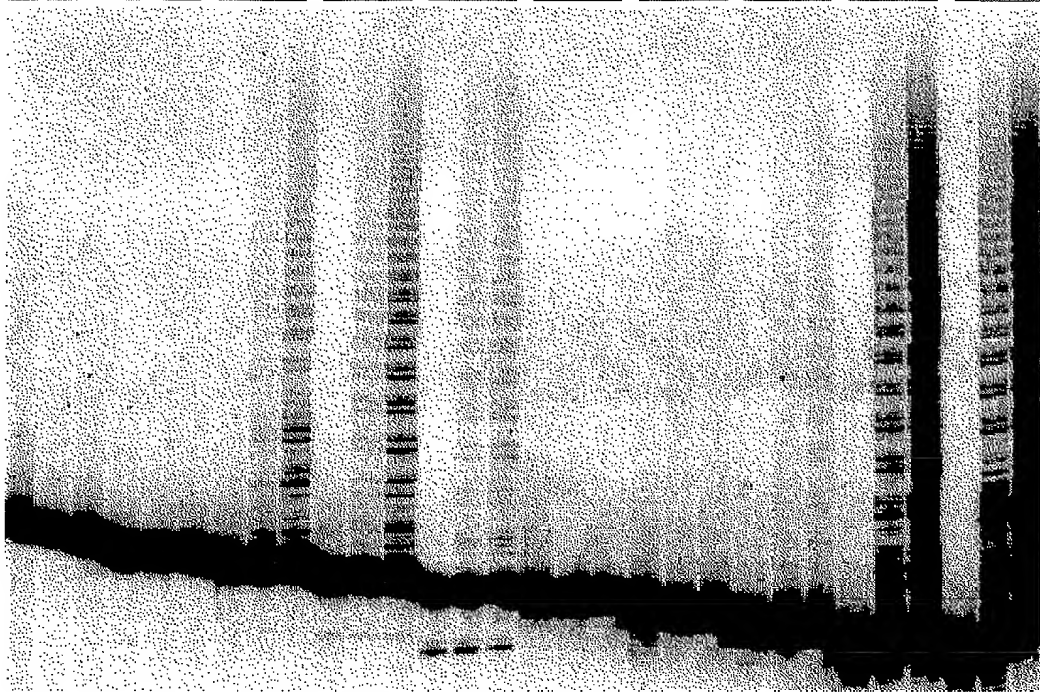
FIG. 30



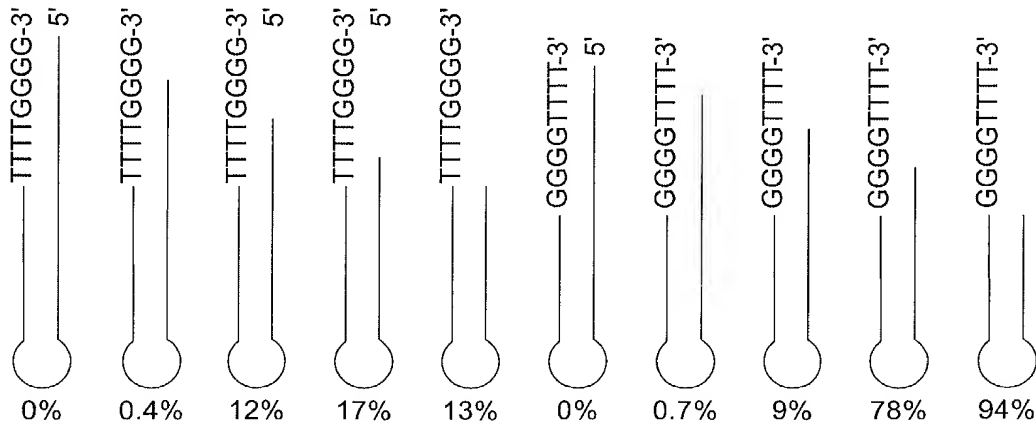
39/103

Telomerase:

+	+	+	+	+	+	+	+	+	+
+	+	+	+	+	+	+	+	+	+
-	+	+	-	+	-	+	-	+	-

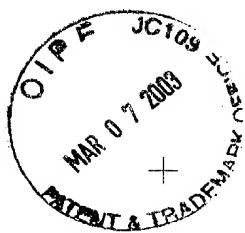


1-3    4-6    7-9    10-12    13-15    16-18    19-21    22-24    25-27    28-30



% primer extended

FIG. 31



40/103

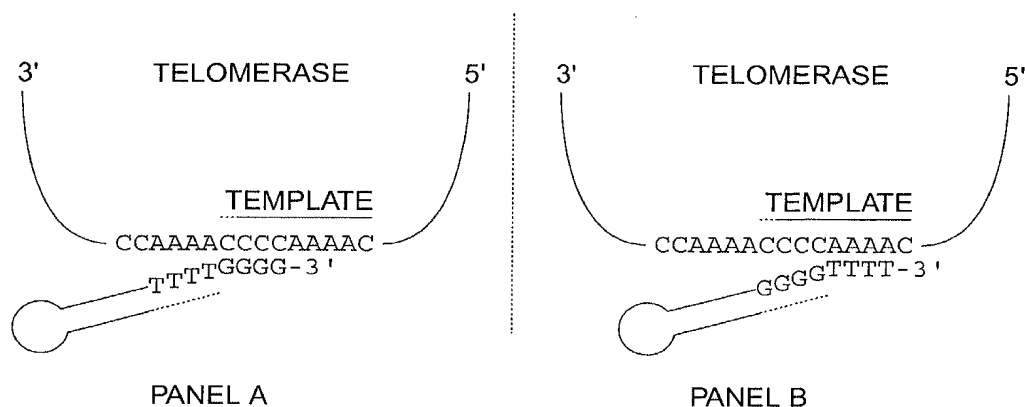


FIG. 32

1	CCCCAAAACC	CCAAAACCCC	AAAACCCCTA	TAAAAAAGA	AAAAATTGAG
51	GTAGTTTAGA	AATAAAATAT	TATTCCTGCA	CAAATGGAGA	TGGATATTGA
101	TTTGGATGAT	ATAGAAAATT	TACTTCCTAA	TACATTCAAC	AAGTATAGCA
151	GCTCTTGTAG	TGACAAGAAA	GGATGCAAAA	CATTGAAATC	TGGCTCGAAA
201	TCGCCTTCAT	TGACTATTCC	AAAGTTGCAA	AAACAATTAG	AGTTCTACTT
251	CTCGGATGCA	AATCTTTATA	ACGATTCCTT	CTTGAGAAAA	TTAGTTTTTAA
301	AAAGCGGAGA	GCAAAGAGTA	GAAATTGAAA	CATTACTAAT	GTTTAAATAA
351	AATCAGGTAA	TGAGGATTAT	TCTATTTTTT	AGATCACTTC	TTAAGGAGCA
401	TTATGGAGAA	AATTACTTAA	TACTAAAAGG	TAAACAGTTT	GGATTATTTT
451	CCTAGCCAAC	AATGATGAGT	ATATTAAATT	CATATGAGAA	TGAGTCAAAG
501	GATCTCGATA	CATCAGACTT	ACCAAAGACA	AACTCGCTAT	AAAACGCAAG
551	AAAAAGTTTG	ATAATCGAAC	AGCAGAAGAA	CTTATTGCAT	TTACTATTCT
601	TATGGGTTTT	ATTACAATTG	TTTTAGGTAT	CGACGGTGAA	CTCCCGAGTC
651	TTGAGACAAT	TGAAAAAGCT	GTTTACAAC	GAAGGAATCG	CAGTTCTGAA
701	AGTTCTGATG	TGTATGCCAT	TATTTTGTGA	ATTAATCTCA	AATATCTTAT
751	CTCAATTTAA	TGGATAGCTA	TAGAAACAAA	CCAAATAAAC	CATGCAAGTT
801	TAATGGAATA	TACGTTAAAT	CCTTTGGGAC	AAATGCACAC	TGAATTTATA
851	TTGGATTCTT	AAAGCATAGA	TACACAGAAT	GCTTTAGAGA	CTGATTTAGC
901	TTACAACAGA	TTACCTGTTT	TGATTACTCT	TGCTCATCTC	TTATATCTTT
951	AAAAGAAGCA	GGCGAAATGA	AAAGAAGACT	AAAGAAAGAG	ATTTCAAAT
1001	TTGTTGATT	TTCTGTAACC	GGAATTAACA	ACAAGAATAT	TAGCAACGAA
1051	AAAGAAGAAG	AGCTATCACA	ATCCTGATT	TTAAAGATTT	CAAAAATTCC
1101	AGGTAAGAGA	GATACATTCA	TTAAAATTCA	TATATTATAG	TTTTTCATTT
1151	CACAGCTGTT	ATTTTCTTTT	ATCTTAACAA	TATTTTTTGA	TTAGCTGGAA
1201	GTAAAAAGTA	TCAAATAAGA	GAAGCGCTAG	ACTGAGGTAA	CCTTAGCTTAT
1251	TCACATTCAT	AGATCGACCT	TCATATATCC	AATACGATGA	TAAGGAAACA
1301	GCAGTCATCC	GTTTTAAAAA	TAGTGCTATG	AGGACTAAAT	TTTTTAGAGTC
1351	AAGAAATGGA	GCCGAAATCT	TAATCAAAAA	GAATTGCGTC	GATATTGCAA
1401	AAGAATCGAA	CTCTAAATCT	TTCGTAAATA	AGTATTACCA	ATCTTGATTG
1451	ATTGAAGAGA	TTGACGAGGC	AACTGCACAG	AAGATCATT	AAGAAATAAA
1501	GTAACTTTTA	TTAATTAGAG	AATAAACTAA	ATTACTAATA	TAGAGATCAG
1551	CGATCTTCAA	TTGACGAAAT	AAAAGCTGAA	CTAAAGTTAG	ACAATAAAAA
1601	ATACAAACCT	TGGTCAAAAT	ATTGAGGAAG	GAAAAGAAGA	CCAGTTAGCA
1651	AAAGAAAAAA	TAAGGCAATA	AATAAAATGA	GTACAGAAGT	GAAGAAATAA
1701	AAGATTTAT	TTTTTCAATA	ATTTATTGAA	AAGAGGGGTT	TTGGGGTTTT
1751	GGGGTTTTGG	GG			

FIG. 34

+



41/103

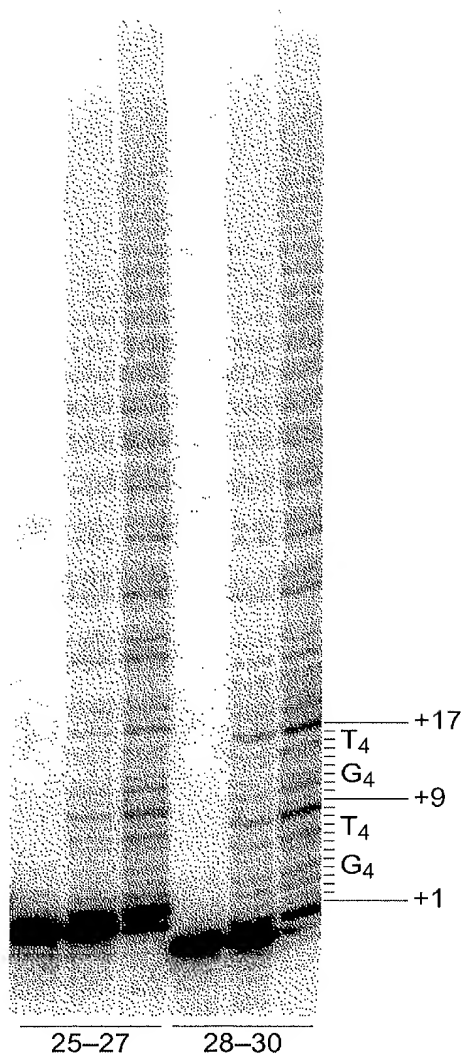
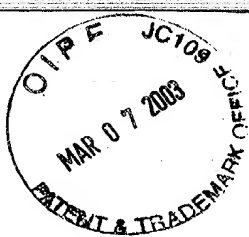


FIG. 33



42/103

CCCCAAAACCCCAAAACCCCAAAACCCCTATAAAAAAGAAAAAATTGAGGTAGTTTAGA  
1 -----+-----+-----+-----+-----+ 60  
GGGGTTTTGGGGTTTTGGGGTTTTGGGGATATTTTTTCTTTTAACTCCATCAAATCT

a P Q N P K T P K P L \* K K K K L R \* F R -  
b P K T P K P Q N P Y K K R K N \* G S L E -  
c P K P Q N P K T P I K K E K I E V V \* K -

AATAAAATATTATTCCTCGCACAAATGGAGATGGATATTGATTGGATGATATAGAAAATT  
61 -----+-----+-----+-----+-----+ 120  
TTATTTTATAATAAGGGCGTGTTCCTCTACCTATAACTAAACCTACTATATCTTTTAA

a N K I L F P H K W R W I L I W M I \* K I -  
b I K Y Y S R T N G D G Y \* F G \* Y R K F -  
c \* N I I P A Q M E M D I D L D D I E N L -

TACTTCCTAATACATTCAACAAGTATAGCAGCTCTTGTAGTGACAAGAAAGGATGCAAAA  
121 -----+-----+-----+-----+-----+ 180  
ATGAAGGATTATGTAAGTTGTTTCATATCGTCGAGAACATCACTGTTCTTCTACGTTTT

a Y F L I H S T S I A A L V V T R K D A K -  
b T S \* Y I Q Q V \* Q L L \* C Q E R M Q N -  
c L P N T F N K Y S S S C S D K K G C K T -

CATTGAAATCTGGCTCGAAATCGCCTTCATTGACTATTCCAAAGTTGCAAAAACAATTAG  
181 -----+-----+-----+-----+-----+ 240  
GTAACCTTAGACCGAGCTTTAGCGGAAGTAAGTGAAGGTTTCAACGTTTTTGTAAATC

a H \* N L A R N R L H \* L F Q S C K N N \* -  
b I E I W L E I A F I D Y S K V A K T I R -  
c L K S G S K S P S L T I P K L Q K Q L E -

AGTTCTACTTCTCGGATGCAAAATCTTTATAACGATTCTTTCTTGAGAAAATTAGTTTTAA  
241 -----+-----+-----+-----+-----+ 300  
TCAAGATGAAGAGCCTACGTTTAGAAATATTGCTAAGAAAGAACTCTTTTAATCAAAATT

a S S T S R M Q I F I T I L S \* E N \* F \* -  
b V L L L G C K S L \* R F F L E K I S F K -  
c F Y F S D A N L Y N D S F L R K L V L K -

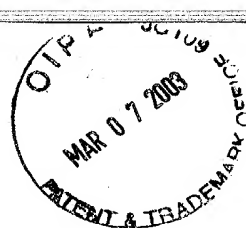
AAAGCGGAGAGCAAAGAGTAGAAATTGAAACATTACTAATGTTTAAATAAAATCAGGTAA  
301 -----+-----+-----+-----+-----+ 360  
TTTCGCCTCTCGTTTCTCATCTTTAACTTTGTAATGATTACAAATTTATTTTAGTCCATT

a K A E S K E \* K L K H Y \* C L N K I R \* -  
b K R R A K S R N \* N I T N V \* I K S G N -  
c S G E Q R V E I E T L L M F K \* N Q V M -

TGAGGATTATTCTATTTTTTAGATCACTTCTTAAGGAGCATTATGGAGAAAATTACTTAA  
361 -----+-----+-----+-----+-----+ 420  
ACTCCTAATAAGATAAAAAATCTAGTGAAGAATTCCTCGTAATACCTCTTTAATGAATT

a \* G L F Y F L D H F L R S I M E K I T \* -  
b E D Y S I F \* I T S \* G A L W R K L L N -  
c R I I L F F R S L L K E H Y G E N Y L I -

FIG. 35



43/103

TACTAAAAGGTAAACAGTTTGGATTATTTCCCTAGCCAACAATGATGAGTATATTAAATT  
421 -----+-----+-----+-----+-----+ 480  
ATGATTTTCCATTTGTCAAACCTAATAAAGGGATCGGTTGTTACTACTCATATAATTTAA

a Y \* K V N S L D Y F P S Q Q \* \* V Y \* I -  
b T K R \* T V W I I S L A N N D E Y I K F -  
c L K G K Q F G L F P \* P T M M S I L N S -

CATATGAGAATGAGTCAAAGGATCTCGATACATCAGACTTACCAAAGACAAACTCGCTAT  
481 -----+-----+-----+-----+-----+ 540  
GTATACTCTTACTCAGTTTCCCTAGAGCTATGTAGTCTGAATGGTTTCTGTTTGAGCGATA

a H M R M S Q R I S I H Q T Y Q R Q T R Y -  
b I \* E \* V K G S R Y I R L T K D K L A I -  
c Y E N E S K D L D T S D L P K T N S L \* -

AAAACGCAAGAAAAAGTTTGATAATCGAACAGCAGAAGAACTTATTGCATTTACTATTTCG  
541 -----+-----+-----+-----+-----+ 600  
TTTTGCGTTCTTTTCAAACCTATTAGCTTGTCGTCCTTGAATAACGTAAATGATAAGC

a K T Q E K V \* \* S N S R R T Y C I Y Y S -  
b K R K K K F D N R T A E E L I A F T I R -  
c N A R K S L I I E Q Q K N L L H L L F V -

TATGGGTTTTATTACAATTGTTTTAGGTATCGACGGTGAACCTCCCGAGTCTTGAGACAAT  
601 -----+-----+-----+-----+-----+ 660  
ATACCCAAAATAATGTTAACAAAATCCATAGCTGCCACTTGAGGGCTCAGAACTCTGTTA

a Y G F Y Y N C F R Y R R \* T P E S \* D N -  
b M G F I T I V L G I D G E L P S L E T I -  
c W V L L Q L F \* V S T V N S R V L R Q L -

TGAAAAAGCTGTTTACAACCTGAAGGAATCGCAGTTCTGAAAGTTCTGATGTGTATGCCAT  
661 -----+-----+-----+-----+-----+ 720  
ACTTTTTTCGACAAATGTTGACTTCTTAGCGTCAAGACTTTCAAGACTACACATACGGTA

a \* K S C L Q L K E S Q F \* K F C C V C H -  
b E K A V Y N \* R N R S S E S S D V Y A I -  
c K K L F T T E G I A V L K V L M C M P L -

TATTTTGTGAATTAATCTCAAATATCTTATCTCAATTTAATGGATAGCTATAGAAACAA  
721 -----+-----+-----+-----+-----+ 780  
ATAAAACACTTAATTAGAGTTTATAGAATAGAGTTAAATTACCTATCGATATCTTTGTTT

a Y F V N \* S Q I S Y L N L M D S Y R N K -  
b I L \* I N L K Y L I S I \* W I A I E T N -  
c F C E L I S N I L S Q F N G \* L \* K Q T -

CCAAATAAACCATGCAAGTTTAAATGGAATATACGTTAAATCCTTTGGGACAAATGCACAC  
781 -----+-----+-----+-----+-----+ 840  
GGTTTATTTGGTACGTTCAAATTACCTTATATGCAATTTAGGAAACCCTGTTTACGTGTG

a P N K P C K F N G I Y V K S F G T N A H -  
b Q I N H A S L M E Y T L N P L G Q M H T -  
c K \* T M Q V \* W N I R \* I L W D K C T L -

TGAATTTATATTGGATTCTTAAAGCATAGATACAGAAATGCTTTAGAGACTGATTTAGC  
841 -----+-----+-----+-----+-----+ 900  
ACTTAAATATAACCTAAGAATTTTCGTATCTATGTGTCTTACGAAATCTCTGACTAAATCG

a \* I Y I G F L K H R Y T E C F R D \* F S -  
b E F I L D S \* S I D T Q N A L E T D L A -  
c N L Y W I L K A \* I H R M L \* R L I \* L -

FIG. 35  
(CONTINUED)



44/103

TTACAACAGATTACCTGTTTTGATTACTCTTGCTCATCTCTTATATCTTTAAAAGAAGCA  
901 -----+-----+-----+-----+-----+ 960  
AATGTTGTCTAATGGACAAAATAATGAGAACGAGTAGAGAATATAGAAATTTTCTTCGT

a L Q Q I T C F D Y S C S S L I S L K E A -  
b Y N R L P V L I T L A H L L Y L \* K K Q -  
c T T D Y L F \* L L L L I S Y I F K R S R -

GGCGAAATGAAAAGAAGACTAAAGAAAGAGATTTCAAAATTTGTTGATTCTTCTGTAACC  
961 -----+-----+-----+-----+-----+ 1020  
CCGCTTTACTTTTCTTCTGATTTCTTTCTCTAAAGTTTTAAACAACTAAGAAGACATTGG

a G E M K R R L K K E I S K F V D S S V T -  
b A K \* K E D \* R K R F Q N L L I L L \* P -  
c R N E K K T K E R D F K I C \* F F C N R -

GGAATTAACAACAAGAATATTAGCAACGAAAAAGAAGAGCTATCACAATCCTGATTCT  
1021 -----+-----+-----+-----+-----+ 1080  
CCTTAATTGTTGTTCTTATAATCGTTGCTTTTTCTTCTTCTCGATAGTGTAGGACTAAG

a G I N N K N I S N E K E E E L S Q S \* F -  
b E L T T R I L A T K K K K S Y H N P D S -  
c N \* Q Q E Y \* Q R K R R R A I T I L I L -

TTAAAGATTTCAAAATTCAGGTAAGAGAGATACATTCATTAATAATTCATATATTATAG  
1081 -----+-----+-----+-----+-----+ 1140  
AATTTCTAAAGTTTTTAAGGTCCATTCTCTCTATGTAAGTAATTTTAAGTATATAATATC

a L K I S K I P G K R D T F I K I H I L \* -  
b \* R F Q K F Q V R E I H S L K F I Y Y S -  
c K D F K N S R \* E R Y I H \* N S Y I I V -

TTTTTCATTTACAGCTGTTATTTTCTTTTATCTTAACAATATTTTTTGATTAGCTGGAA  
1141 -----+-----+-----+-----+-----+ 1200  
AAAAAGTAAAGTGTGCGACAATAAAAGAAAATAGAATTGTTATAAAAACTAATCGACCTT

a F F I S Q L L F S F I L T I F F D \* L E -  
b F S F H S C Y F L L S \* Q Y F L I S W K -  
c F H F T A V I F F Y L N N I F \* L A G S -

GTAAAAAGTATCAAAATAAGAGAAGCGCTAGACTGAGGTAAGTATTCACATTCAT  
1201 -----+-----+-----+-----+-----+ 1260  
CATTTTTTCATAGTTTATTCTCTTCGCGATCTGACTCCATTGAATCGAATAAGTGAAGTA

a V K S I K \* E K R \* T E V T \* L I H I H -  
b \* K V S N K R S A R L R \* L S L F T F I -  
c K K Y Q I R E A L D \* G N L A Y S H S \* -

AGATCGACCTTCATATATCCAATACGATGATAAGGAAACAGCAGTCATCCGTTTTAAAAA  
1261 -----+-----+-----+-----+-----+ 1320  
TCTAGCTGGAAGTATATAGGTTATGCTACTATTCTTTGTCGTCAGTAGGCAAAATTTT

a R S T F I Y P I R \* \* G N S S H P F \* K -  
b D R P S Y I Q Y D D K E T A V I R F K N -  
c I D L H I S N T M I R K Q Q S S V L K I -

TAGTGCTATGAGGACTAAATTTTGTAGAGTCAAGAAATGGAGCCGAAATCTTAATCAAAAA  
1321 -----+-----+-----+-----+-----+ 1380  
ATCACGATACTCCTGATTTAAAAATCTCAGTTCTTTACCTCGGCTTTAGAATTAGTTTT

a \* C Y E D \* I F R V K K W S R N L N Q K -  
b S A M R T K F L E S R N G A E I L I K K -  
c V L \* G L N F \* S Q E M E P K S \* S K R -

FIG. 35  
(CONTINUED)





45/103

1381 GAATTGCGTCGATATTGCAAAAGAATCGAACTCTAAATCTTTCGTTAATAAGTATTACCA -  
-----+-----+-----+-----+-----+ 1440  
CTTAACGCAGCTATAACGTTTTCTTAGCTTGAGATTAGAAAAGCAATTATTCATAATGGT

a E L R R Y C K R I E L \* I F R \* \* V L P -  
b N C V D I A K E S N S K S F V N K Y Y Q -  
c I A S I L Q K N R T L N L S L I S I T N -

1441 ATCTTGATTGATTGAAGAGATTGACGAGGCAACTGCACAGAAGATCATTAAGAAATAAA  
-----+-----+-----+-----+-----+ 1500  
TAGAACTAACTAACTTCTCTAACTGCTCCGTTGACGTGTCTTAGTAATTTCTTTATTT

a I L I D C R D C R G N C T E D H \* R N K -  
b S \* L I E E I D E A T A Q K I I K E I K -  
c L D \* L K R L T R Q L H R R S L K K \* S -

1501 GTAACTTTTATTAAATTAGAGAATAAACTAAATTACTAATATAGAGATCAGCGATCTTCAA  
-----+-----+-----+-----+-----+ 1560  
CATTGAAAATAATTAATCTCTTATTTTGATTTAATGATTATATCTCTAGTCGCTAGAAGTT

a V T F I N \* R I N \* I T N I E I S D L Q -  
b \* L L L I R E \* T K L L I \* R S A I F N -  
c N F Y \* L E N K L N Y \* Y R D Q R S S I -

1561 TTGACGAAATAAAAGCTGAACTAAAGTTAGACAATAAAAAATACAAACCTTGGTCAAAT  
-----+-----+-----+-----+-----+ 1620  
AACTGCTTTATTTTCGACTTGATTTCAATCTGTTATTTTTATGTTTGGAAACCAGTTT

a L T K \* K L N \* S \* T I K N T N L G Q N -  
b \* R N K S \* T K V R Q \* K I Q T L V K I -  
c D E I K A E L K L D N K K Y K P W S K Y -

1621 ATTGAGGAAGGAAAAGAAGACCAGTTAGCAAAAGAAAAATAAGGCAATAAATAAATGA  
-----+-----+-----+-----+-----+ 1680  
TAACTCCTTCCTTTTCTTCTGGTCAATCGTTTTCTTTTATTCCGTTATTTATTTTACT

a I E E G K E D Q L A K E K I R Q \* I K \* -  
b L R K E K K T S \* Q K K K \* G N K \* N E -  
c \* G R K R R P V S K R K N K A I N K M S -

1681 GTACAGAAGTGAAGAAATAAAAGATTTATTTTTTTCAATAATTTATTGAAAAGAGGGGTT  
-----+-----+-----+-----+-----+ 1740  
CATGTCTTCACTTCTTTATTTTCTAAATAAAAAAAGTTATTAAATAACTTTTCTCCCCAA

a V Q K \* R N K R F I F F N N L L K R G V -  
b Y R S E E I K D L F F S I I Y \* K E G F -  
c T E V K K \* K I Y F F Q \* F I E K R G F -

1741 TTGGGGTTTTGGGGTTTTGGGG  
-----+-----+-----+-----+ 1762  
AACCCCAAACCCCAAACCCC

a L G F W G F G -  
b W G F G V L G -  
c G V L G F W -

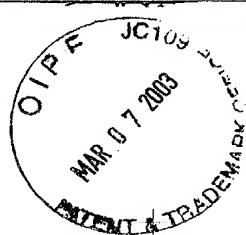
FIG. 35  
(CONTINUED)

FIG. 36





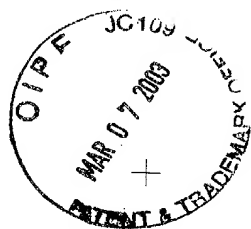
FIG. 42



50/103

Motif A		Motif B
Consensus telomerase p123 Dong (LINE) a1 S.c. (group II) HIV-RT L8543.12	h--hDh--h--h GQPKLFFATMDIEKCYDSVNREKLSFLKTTKLL-100-KFYKQTKGIPQGLCVSSILSSFFYYATIEESSLGFL KNRNHCTYDDYKKAFDSPHSWLIQVLEIYKIN-28-RQIAIKKGIYQGDSISPLWFCALNPLSHQLHNR FGGSNWFREVDLKKCFDTISHDLIIKELKRYISD-26-HVPVGPVVCVQGAPTSALCNVALLRDLRRLAGLA LKKKKSVTVLVGDAYFSVPLDEDFRKYTAFTIP-7-GIRYQYNVLPQGWKGSPIFQSSMTKILEPFRKQN VLPELYFMKFDVKSCYDSIPRMECNRILKDALKN-68-KCYTREDGLFQGSLSAPIVDLVYDDLLLEFYSEFK	h----+QG---SP
Motif C		Motif D
Consensus telomerase p123 Dong (LINE) a1 S.c. (group II) HIV-RT L8543.12	h--YhDdhhh -14-LMRLTDDYLLITTQENN-0-AVLFIKLIINVSRENGKFNMKLQT-23-QDYCDWIGISI -16-HLIYMDIDIKLYAKNDKE-0-MKKLIDTTTIFSNDSIMQFGLDKCT-25-KCLYKYLGFQQ -55-YVRYADDLIGVLGSKN-2-KIIRDLNNFLNS.IGLTINEKTLI-4-ETPARFLGYNI -4-IYQYMDLIVVGSHEIG-1-HRTKIEELRQHLRWGLTTPDKKHQK-0-EPPFLWMGYEL -8-ILKLADDFLIISTDQQQ.....VINIKKLAMGGFQKYNKANR-41-IRSKSSKGIPIR	h-hLgh-h

FIG. 40



51/103

MEIENNQAQQPKAEKLWWELELEMQENQNDIQVRVKIDDPKQYL  
VNVTAACLLQEGSYQDKDERRYIITKALLEVAESDPEFICQLA  
VYIRNELYIRTTTNYIVAFVVKNTQPFIEKYFNKAVLLPNDL  
LEVCEFAQVLYIFDATEFNLYLDRILSQDIRKELTRKCLQRC  
VRSKFSEFNEYQLGKYCTESQQRKKTMTFRYLSVTNKQKWDQTKKK  
RKENLLTKLQAIKESSEDKSKRETGDIMNVEDAIKALKPAVMKKI  
AKRQONAMKKHMKAPKIPNSTLESKYLTFKDLIKFCHISEPKERV  
YKILGKKYPKTEEEYKAAFSDSASAPFNPELAGKRMKIEISKTW  
ENELSAKGNTAEVWDNLISSNQLPYMAMLRNLSNILKAGVSDTT  
HSIVINKICEPKAVENSKMFPLQFFSAIEAVNEAVTKGFKAKKR  
ENMNLKGQIEAVKEVVEKTDDEKKDMELEQTEEGEFVKVNEGIG  
KQYINSIELAIIKIAVNKNLDEIKGHTAIFSDVSGSMSTSMSSGA  
KKYGSVRTCLECALVGLMVKQRCCKSSFYIFSSPSSQCNKCYL  
EVDLPGLDELPSMQKLLQEKGLGGGTDFFPYECIDEWTKNKT  
DNIVILSDMMIAEGYSDINVRGSSIVNSIKKYKDEVNPNIKIFA  
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VEVIKNFALQKIGQK

FIG. 43

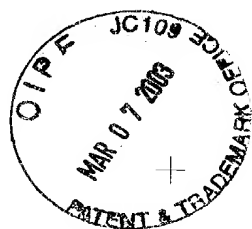
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QVQLIKKVGSKVEKDLNLNEDENKKNGLSEQQVKEEQLRTITTEE  
QVKYQNLVFNMDYQLDLNESGGHRRHRRETDDYDEKWFIEISHDQ  
KNYVSIYANQKTSYCWWLKDYFNKNNDYHNLVNSINRLETEAEFY  
AFDDFSQTIKLTNNSYQTVNIDVNFNNLCILALLRFLLSLERF  
NILNIRSSYTRNQYNFEKIGELLETFIVVFSHRHLQGIHLQVP  
CEAFQYLVNSSSQISVKDSQLQVYSFSTDCLKLVDTNKVQDYFKF  
LQEFPRLTHVSQQAIPVSATNAVENLNVLLKKVKHANLNLVSI  
TQFNDFYFVNLQHLKLEFGLLEPNILTKQKLENLLLSIKQSKNL  
KFLRLNFYTYVAQETSRKQILKQATTIKNLKNNKNQEETPETKD  
ETPSESTSGMKFFDHLSELTELEDFSVNLQATQEIYDSLHKLII  
RSTNLKKFKLSYKYEMEKSKMDTFIDLKNIYETLNNLKRCVSNI  
SNPHGNISYELTNKDSTFYKFKLTNLQELQHAKYTFKQNEFQFN  
NVKSAKIESSSLESLEDIDSLCKSIASCNNLQNVNIIASLLYPN  
NIQKNPFNKPNLLFFKQFEQLKNLENVSINCILDQHIILNSISEF  
LEKNKKIKAFILKRYLLQYYLDYTKLFTLQQLPELNQVYINQ  
QLEELTVSEVHKQVWENHKQKAFYEPLCEFIKESSQTLQLIDFD  
QNTVSDDSIKKILESISESKYHHYLRNLNPSQSSSLIKSENEEIQ  
ELLKACDEKGVLVKAYYKFPLCLPTGTYYDYNSDRW

FIG. 45

MKILFEFIQDKLDIDLQTNSTYKENLKCGLHFNGLDEILTTCPAL  
PNSRKIALPCLPGDLSHKAVIDHCIYLLTGELYNVLTFGYKI  
ARNEDVNNSLFCHSANVNVTLKGAAWKMFHSLVGYAFVDLLI  
NYTVIQFNGQFFTQIVGNRCNEPHLPKQVWQSSSSSATAAQIK  
QLTEPVTNKQFLHKLINSSSFFPYSKILPSSSSIKKLTDLREA  
IFPTNLVKIPQRLKVRINLTQKLLKRHKRLNYSILNSICPPL  
EGTVLDLSHLRSQSPKERVLFKFIIVILQKLLPQEMFGSKKNKGK  
IIKNLNLSSLPPLNGYLPFDSLLKKLRLKDFRWLFISDIWFTKH  
NFENLNQLAICFISWLFRLIPKIIQTFYCYTEISSTVTIVYFR  
HDTWNKLITPFIVEYFKTYLVENNVCRNHNSYTLNFNHNSKMRI  
IPKKSNNEFRIIAIPCRGADEEEFTIYKENHNKNAIQPTQKILEY  
LRNKRPTSFTKIYSPTQIADRIKEFKQRLKKFNNVLPPELYFMK  
FDVKSCYDSIPRMECMRILKDALKNENGFFVRSQYFFNTNTGVL  
KLFNVVNASRVKPYELYIDNVRTVHLSNQDVINVVEMEIFKTA  
LWVEDKCYIREDGLFQGSLSAPIVDLVYDDLLEFYSEFKASPS  
QDTLILKLADDFLIISTDQQQVINIKKLAMGGFQKYNANARNDK  
ILAVSSQSDDDTVIQFCAMHIFVKELEVWKHSSTMNNFHIRSKS  
SKGIFRSLIALFNTRISYKTIDTNLNSTNTVLMQIDHVVKNISE  
CYKSAFKDLSINVTQNMQFHSFLQRIIEMTVSGCPITKCDPLIE  
YEVRFTILNGFLESLSNNTSKFKDNIILLRKEIQHLQAYIYIYI  
HIVN

FIG. 46

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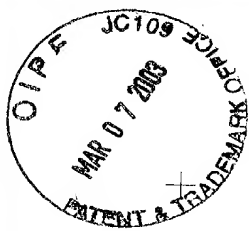


52/103

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1 tcaatactat taattaataa ataaaaaaaa gcaaactaca aagaaaatgt caaggcgtaa
61 ctaaaaaaag ccataggctc ctataggcaa tgaaacaaat cttagttttg tattacaaaa
121 tctagaagtt tacaaaagcc agattgagca ttataagacc tagtagtaat agatcaaaga
181 ggaggatctc aagcttttaa agttcaaaaa ttaagattag gatggaaaact ctggcaacga
241 tgatgatgat gaagaaaaca actcaataaa ataataagaa ttattaagga gagtcaatta
301 gattaagtag caagtttaat tgataaaaaa agttggttct aaggtagaga aagatttgaa
361 tttgaacgaa gatgaaaaca aaaagaatgg actttctgaa tagcaagtga aagaagagta
421 attaagaacg attactgaag aataggttaa gtattaaaat ttagtattta acatggacta
481 ccagttagat ttaaattgaga gtgggtggcca tagaagacac agaagagaaa cagattatga
541 tactgaaaaa tggtttgaaa tatctcatga ccaaaaaaat tatgtatcaa tttacgccaa
601 ctaaaagaca tcatattggt ggtggcctaa agattatttt aataaaaaaca attatgatca
661 tcttaattgta agcattaaca gactagaaac tgaagccgaa ttctatgcct ttgatgattt
721 ttcacaaaaca atcaaaactta ctaataattc ttactagact gttaacatag acgttaattt
781 tgataaataat ctctgtatac tgcattgct tagattttta ttatcactag aaagattcaa
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901 gctacttgaa actatcttcg cagttgtctt ttctcatcgc cacttacaag gcattcattt
961 acaagttcct tgcgaagcgt tctaattttt agttaactcc tcatcataaa ttagcgttaa
1021 agatagctaa ttatagggtat actctttctc tacagactta aaattagttg acactaacaa
1081 agtccaagat ttttttaagt tcttataaga attccctcgt ttgactcatg taagctagta
1141 ggctatccca gtttagtgcta ctaacgcgtg agagaacctc aatgttttac ttaaaaaggtt
1201 caagcatgct aatcttaatt tagtttctat ccttacctaa ttcaattttg atttctactt
1261 tgttaattta taacatttga aattagagtt tggattagaa ccaaatattt tgacaaaaca
1321 aaagcttgaa aatctacttt tgagtataaa ataatacaaaa aatcttaaat ttttaagatt
1381 aaacttttac acctacggtt cttaaagaaac ctccagaaaa cagatattaa aacaagctac
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1561 gcttgaagat ttcagcggtt acttgtaagc tacccaagaa atttatgata gcttgcacaa
1621 acttttgatt agatcaacaa atttaaagaa gttcaaatat agttacaaat atgaaatgga
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1981 aaatttacaa aatgttaata ttatcgccag ttgctctat cccaacaata ttagaaaaaa
2041 tcttttcaat aagcccaatc ttctattttt caagcaattt gaataattga aaaatttgga
2101 aaatgtatct atcaactgta ttcttgatca gcatatactt aattctattt cagaattctt
2161 agaaaagaat aaaaaaataa aagcattcat tttgaaaaga tattatttat tacaatatta
2221 tcttgattat actaaattat ttaaaacact tcaatagtta cctgaattaa attaagttta
2281 cattaattag caattagaag aattgactgt gagtgaagta cataagtaag tatgggaaaa
2341 ccacaagcaa aaagctttct atgaaccatt atgtgagttt atcaaagaat catcctaaac
2401 ccttttagcta atagattttg accaaaacac tgtaagtgat gactctatta aaaagatttt
2461 agaactata tctgagtcta agtatcatca ttatttgaga ttgaacccta gttaatctag
2521 cagtttaatt aaatctgaaa acgaagaaat ttaagaactt ctcaaagctt ggcacgaaaa
2581 aggtgtttta gtaaaagcat actataaatt cctctatagt ttaccaactg gtacttatta
2641 cgattacaat tcagatagat ggtgattaat taaatattag tttaaataaa tattaatat
2701 tgaatatttc tttgcttatt atttgaataa tacatacaat agtcattttt agtgttttga
2761 atatatttta gttattttaat tcattatttt aagtaataaa ttatttttca atcatttttt
2821 aaaaaatcg
```

FIG. 44





53/103

Oxytricha  
Euplotes

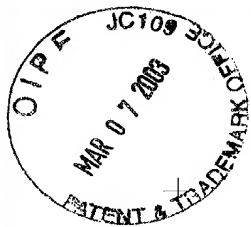
LCVSYILSSFYYANLEENALQFLRKESMDPEKPETNLLMRLT  
LCVSSILSSFYYATLEESSLGFLRDESMNPENPNVNLLMRLT

FIG. 47

ATTTATACTCATGAAAATCTTATTCGAGTTCATTCAAGACAAGCTTGACATTGATCTACA  
GACCAACAGTACTTACAAAGAAAATTTAAATGTGGTCACTTCAATGGCCTCGATGAAAT  
TCTAACTACGTGTTTCGCACTACCAAATTCAGAAAAATAGCATTACCATGCCTTCCTGG  
TGACTTAAGCCACAAAGCAGTCATTGTACTGTCATCATTTACCTGTTGACGGGCGAATT  
ATACAACAACGTACTAACATTTGGCTATAAAATAGCTAGAAATGAAGATGTCAACAATAG  
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GTTCCACAGTTTGGTCCGTACATACGCATTTCGTTGATTTATTGATCAATTATACAGTAAT  
TCAATTTAATGGGCAGTTTTTCACTCAAATCGTGGGTAACAGATGTAACGAACCTCATCT  
GCCGCCAAATGGGTCCAACGATCATCCTCATCATCCGCAACTGCTGCGCAAATCAAACA  
ACTTACAGAACCAGTGACAAATAAACCAATTCCTTACACAAGCTCAATATAAAATTCCTCTTC  
TTTTTTTTCTTATAGCAAGATCCTTCCTTCATCATCATCTATCAAAAAGCTAACTGACTT  
GAGAGAAGCTATTTTTCCCACAAATTTGGTTAAAAATTCCTCAGAGACTAAAGGTACGAAT  
TAATTTGACGCTGCAAAAGCTATTTAAAGAGACATAAGCGTTTGAATTACGTTTCTATTTT  
GAATAGTATTTGCCCCACCATTGGAAGGGACCGTATTGGACTTGTGCGCATTTGAGTAGGCA  
ATCACCAAAGGAACGAGTCTTGAAATTTATCATTTGTTATTTTACAGAAGTTATTACCCCA  
AGAAATGTTTGGCTCAAAGAAAAATAAAGGAAAAATTTATCAAGAATCTAAATCTTTTATT  
AAGTTTACCCTTAAATGGCTATTTACCATTGATAGTTTGTGAAAAAGTTAAGATTAA  
GGATTTTTCGGTGGTTGTTTCAATTTCTGATATTTGGTTCACCAAGCACAAATTTGAAAACCTT  
GAATCAATTGGCGATTTGTTTCAATTTCTGGCTATTTAGACAACCTAATTCCTCAAAATTTAT  
ACAGACTTTTTTTTACTGCACCGAAATATCTTCTACAGTGACAATTGTTTACTTTAGACA  
TGATACTTGGAAATAAACTTATCACCCCTTTTATCGTAGAATATTTTAAAGACGTACTTAGT  
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AGGGGCGAGACGAAGAAGAATTCACAATTTATAAGGAGAATCACAAAAATGCTATCCAGCC  
CACTCAAAAAATTTTAGAATACCTAAGAAACAAAAGGCCGACTAGTTTTACTAAAAATATA  
TTCTCCAACGCAAATAGCTGACCGTATCAAGAATTTAAGCAGAGACTTTTAAAGAAATTT  
TAATAATGTCTTACCAGAGCTTTATTTTATGAAATTTGATGTCAAATCTTGCTATGATTC  
CATACCAAGGATGGAATGTATGAGGATACTCAAGGATGCGCTAAAAAATGAAATGGGTT  
TTTCGTTAGATCTCAATATTTCTTCAATACCAATACAGGTGTATTGAAGTTATTTAATGT  
TGTTAACGCTAGCAGAGTACCAAAACCTTATGAGCTATACATAGATAATGTGAGGACGGT  
TCATTTATCAAATCAGGATGTTATAAACGTTGTAGAGATGGAAATATTTAAACAGCTTT  
GTGGGTTGAAGATAAGTGCTACATTAGAGAAGATGGTCTTTTTTCAGGGCTCTAGTTTATC  
TGCTCCGATCGTTGATTTGGTGTATGACGATCTTCTGGAGTTTTATAGCGAGTTTAAAGC  
CAGTCCTAGCCAGGACACATTAATTTTAAACTGGCTGACGATTTCTTTATAATATCAAC  
AGACCAACAGCAAGTGATCAATATCAAAAAGCTTGCCATGGGCGGATTTCAAAAATATAA  
TGCGAAAGCCAATAGAGACAAAATTTAGCCGTAAGCTCCCAATCAGATGATGATACGGT  
TATTCATTTTGTGCAATGCACATATTTGTTAAAGAATTGGAAGTTTGGAAACATTCAAG  
CACAATGAATAATTTCCATATCCGTTGAAATCTAGTAAAGGGATATTTCAAGTTTAAAT  
AGCGCTGTTTAAACACTAGAATCTCTTATAAAACAATTGACACAAATTTAAATTTCAACAAA  
CACCGTTCTCATGCAAATGATCATGTTGTAAAGAACATTTGGAATGTTATAAATCTGC  
TTTTAAGGATCTATCAATTAATGTTACGCAAAATATGCAATTTTATTGCTTCTTACAACG  
CATCATTGAAATGACAGTCAGCGGTTGTCCAATTACGAAATGTGATCCTTTAATCGAGTA  
TGAGGTACGATTACCATATTGAATGGATTTTTTGGAAAGCCTATCTTCAACACATCAAA  
ATTTAAAGATAATATCATTCTTTTGAAGAAAGAAATTCACACTTGCAAGC

FIG. 48

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54/103

AKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKS VWSKLQSIGIRQHLKR  
VQLRDVSEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNDYVVGARTFRREK  
RAERLTSRVKALFSVLNYERA

FIG. 49

GCCAAGTTCCTGCACTGGCTGATGAGTGTGTACGTCGTCGAGCTGCTCAGGTC  
TTTTCTTTTATGTCACGGAGACCACGTTTCAAAAGAACAGGCTCTTTTTCTACC  
GGAAGAGTGTCTGGAGCAAGTTGCAAAGCATTGGAATCAGACAGCACTTGAAG  
AGGGTGCAGCTGCGGGACGTGTCGGAAGCAGAGGTCAGGCAGCATCGGGAAGC  
CAGGCCCCGCTGCTGACGTCCAGACTCCGCTTCATCCCCAAGCCTGACGGGC  
TGCGGCCGATTGTGAACATGGACTACGTGTCGTCGGGAGCCAGAACGTTCCGCAGA  
GAAAAGAGGGCCGAGCGTCTCACCTCGAGGGTGAAGGCACTGTTTCAGCGTGT  
CAACTACGAGCGGGCGCG

FIG. 50

MTEHHTPKSRILRFLENQYVYLCTLNDYVQLVLRGSPASSYSNICERLRSDVQTSFSIFLHSTVVGF  
DSKPDEGVQFSSPKCSQSELIANVVKQMFDESFERRRNLLMKGFMSNHEDFRAMHVNGVQNDLVSTF  
PNYLISILESKNWQLLEIIGSDAMHYLLSKGSIFEALPNDNYLQISGIPLFKNNVFEE TVSKKRKR  
TIETSITQNK SARKEVSWNSISISRFSIFYRSSYKKFKQDLYFNLHSICDRNTVHMLQWIFPRQFG  
LINAQVVKQLHKVIPLVSQSTVVPKRLLKVYPLIEQTAKRLHRISLSKVYNHYCPYIDTHDDEKILS  
YSLKPNQVFAFLRSILVRVFPKLIWGNQRIFEIILKDLETFLKLSRYESFSLHYLMSNIKISEIEWL  
VLGKRSNAKMCLSDFEKRKQIFAEFIYWLNSFIIPILQSFFYITESSDLNRNTVYFRKDIWLLCR  
PFITSMKMEAF EKINENNVRMDTQKTTLP PAVIRLLPKKNTFRLITNLRKRFLIKMGSNKKMLVSTN  
QTLRPVASILKHLIN EESSGIPFNLEVYMKLLTFKKDLLKHRMFGRKKYFVRIDIKSCYDRIKQDLM  
FRIVKKKLKDPEFVIRKYATIHATSDRATKNFVSEAFSYFDMVPFEKVQVLLSMKTSDTL FVDFVDY  
WTKSSSEIFKMLKEHLSGHIVKIGNSQYLQKVGI PQGSILSSFLCHFYMEDLIDEYLSFTKKKGSVL  
LRVVD DFLFITVNKKDAKKFLNLSLRGF EKHNFTSLEKTVINFENSNGIINNTFFNESKKRMPFFG  
FSVNMRLD TLLACPKIDEALFNSTSVELTKHMGKSFFYKILRSSLASFAQVFIDITHNSKFNSCCN  
IYRLGYSMCMRAQAYLKRMDIFIPQRMFITDLLNVIGRKIWKKLAEILGYTSRRFLSSAEVKWLF C  
LGMRDGLKPSFKYHPCFEQLIYQFQSLTDLIKPLRPVLRQVFLHRR IAD

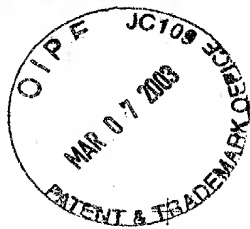
FIG. 51





TTCTTACTTTTAAAGAGGATCTTCTTAAGCACCGAATGTTTTGGgtaattataataatgcgagattccctcattattaatttt  
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GTTAAAGAAACTCAAGGATCCCGAATTTGTAATTCGAAGATGATCAACATACATGCAACAAGTGACCGAGCTACAAA  
AAACTTTGTAGTGAGGCGTTTCTATTgttaagtttattttttcatgggaattttttaaacaattcttttttagTTGAT  
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GACCAAAAGTTCTTCTGAATTTTAAATGCTCAAGGAACATCTCTCTGGACACATTTGTTAAGgtataaccaattgtga  
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AGCTGACGAAACATATGGGAAATCTTTTGTACAAAATCTAAAGgtatctgtgaactgaataaatagctgacaaata  
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AATTTGGAAGAAAGTTGGCCGAAATATTAGGATATACGAGTAGGCGTTTCTGTCTCTGCAAGATCAAAATGtactgt  
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gttattagtttgattgagttgcttttactataactttaagaaagattgacagtggttgctgactactgcccacatg  
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agtttgataactaataagctaatttaatgtcttataaagtttttggtttctcctgacttcaatttgcagtggtgaaaag  
aaatagtgtaagccattattggattccgaaatagccaaatttcttggttcccaagcgggaagtcataagaaactattg  
aagcttatgaggtctcaaaactcctcctgatttaagagggaatcttccaccgtagaggaaatggatagcttatcagct  
gctgagggaagccataatttggcaaaaagaaaatcatctgggagacatctcttggaatcagatgoggagagat  
ctccagcggatccttgatgtcaataacttctatttctgaaatgatggtcctactgtcgtctcagacttctcgtagctcta  
cgcagttaagtgacccaaaggtacc

FIG. 52  
(CONTINUED)



57/103

EST2 pep	FFYCTEISST VTIVYFRHDT WN-----KLIT P-----FIVE YPK-TYLVEN	40
Euplotes pep	FFYVTEQOKS YSKTYYYRKN IWDVI-MKMS IAD-----LKK ETLA--EVQE	43
Trans of tetrahymen	-----KHKE GSQIFYRKP IWKLVSCLTI VKVRIQFSEK NKQMKNNFYQ	44
Consensus	FFY.TE..K..S...YYRK. IW....-KL.. ....-F..K .....	50
EST2 pep	NVCRNHSY- ----- TLSNFHNSKM RUIPKKSNE FRPIAIPCRG	79
Euplotes pep	KEVEEWKKS L ----- GFAPGKG RLIPKKT-- FRPIMTFNKK	78
Trans of tetrahymen	KIQLEENLE KVEEKLIPED SFQYPOGKL RUIPKKS-- FRPIMTFNRK	92
Consensus	K...E..... ----- F..GKL RUIPKK.... FRPIMTF.RK	100
EST2 pep	ADEEFTIYK ENHKNAIQPT QKILEYLRNK RPTSFTKIYS PTQIADRIKE	129
Euplotes pep	IVNSDRKTTK LTTNTKLINS HMLKTLKN- -----RMFK -DPFGFAVFN	120
Trans of tetrahymen	DKQKNIK--- LNLNQILMDS QLVFRNLKD- -----ML-G -QKIGYSVFD	130
Consensus	.....K..K LN.N..L..S QL.L..LKN- ----- ..IG..VF.	150
EST2 pep	FKQRLIKKFN NVL----- PLYFMKFD VKSCYD	157
Euplotes pep	YD-DVMKKYE EFVCKWKQVH CPKLFATMD IEKCYD	155
Trans of tetrahymen	NK-QISEKFA QFIEKWKNG RPLYYVTL- -----	158
Consensus	.K....KKF. .F..KWK..G .P.LYF.T.D ...CYD	186

FIG. 53



58/103

S-1: FFY VTE TTF QKN RLF FYR KSV WSK  
 S-2: RQH LKR VQL RDV SEA EVR QHR EA  
 S-3: ART FRR EKR AER LTS RVK ALF SVL NYE

A-1: AKF LHW LMS VYV VEL LRS FFY VTE TTF Q  
 A-2: LFF YRK SVW SKL QSI GIR QHL KRV QLR DVS  
 A-3: PAL LTS RLR FIP KPD GLR PIV NMD YVV

*FIG. 54*

Poly 4

5' - <sup>t</sup> c a g c c t c g <sup>t</sup> <sup>c</sup>  
 cag acc aaa gga att cca taa gg -3'  
 Q T K G I P Q G

4 (B')

5 (c')

<sup>D</sup> <sup>D</sup> <sup>Y</sup> <sup>L</sup> <sup>L</sup> <sup>I</sup> <sup>T</sup>  
 3' - ctg ctg atg gag gag tag tgg -5'  
 a a a a a a a a  
 t t t t  
 c c  
Poly 1

*FIG. 56*

+



59/103

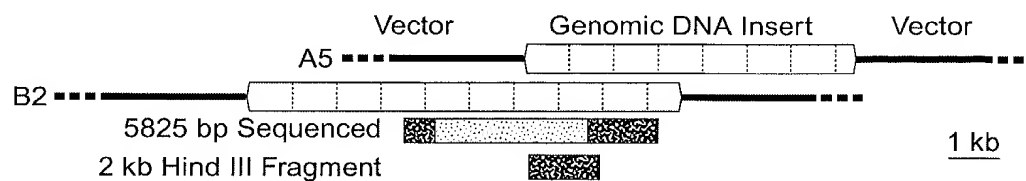


FIG. 55A

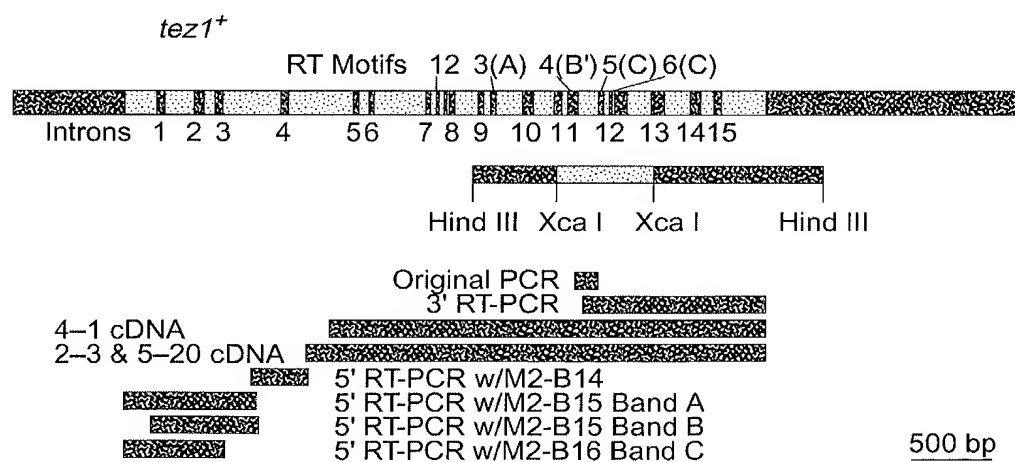


FIG. 55B



60/103

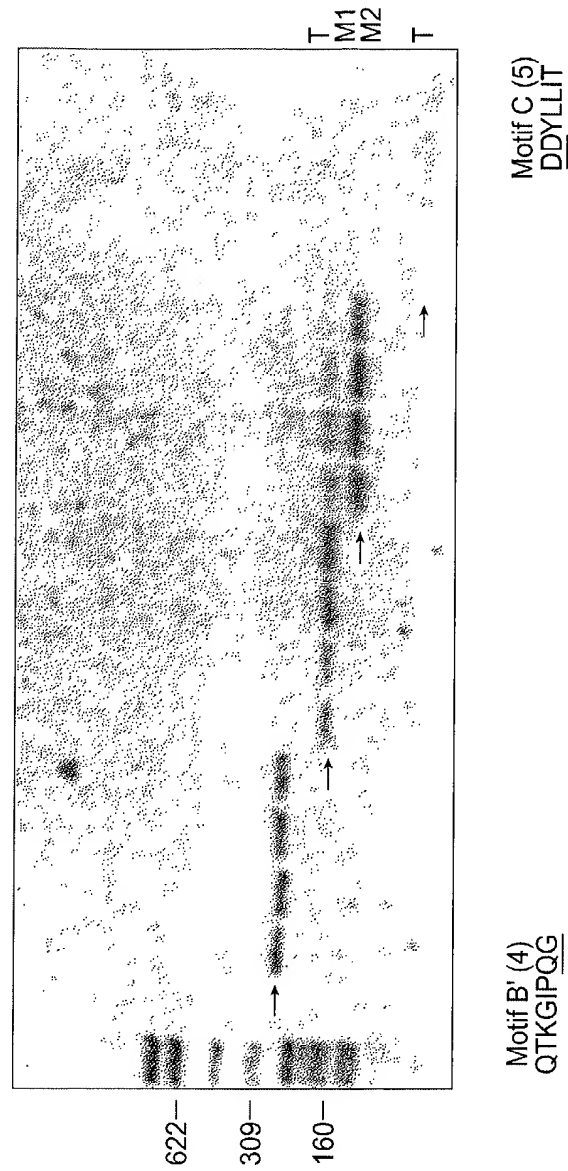
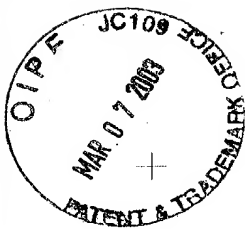


FIG. 57





61/103

Ot LCVSYILSSFYANLEENALQFLRKESMDPEKPEKNLLMRLT  
Fa\_p123 KGIPQGLCVSSILSSFYATLEESSLGFLRDESMNPENPNVNLMLRLTDDYLLIT  
Sp\_M2 SILSSFLCHFYMEDLIDEYLSFTKKK-----GSVLLRVV  
Sc\_p103 DGLFQGGSSLSAPIVDLVYDDLLLEFYSEFKASPS-----QDTLILKLADDFLIIS  
\* . . \* . \* . . . . .

Q K V G I P Q G  
caa aaa gtt ggt atc cct cag gg..... <----Actual Genomic Sequence.

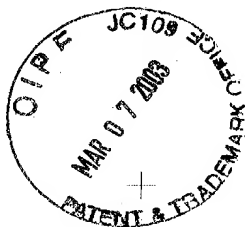
Poly 4  
t t c

t a a g c c t c g  
cag acc aaa gga att cca taa gg ---->

ag acc aaa gga att cca tca ggc tca att ctg tca tct ttt ttg tgt cat ttc tat atg  
tc tgg ttt cct taa ggt agt ccg agt taa gac agt aga aaa aac aca gta aag ata tac

K G I P S G S I L S S F L C H F Y M

FIG. 58



62/103

GAA GAT TTG ATT GAT GAA TAC CTA TCG TTT ACG AAA AAG AAA GGA TCA GTG TTG TTA CGA  
CTT CTA AAC TAA CTA CTT ATG GAT AGC AAA TGC TTT TTC TTT CCT AGT CAC AAC AAT GCT  
E D L I D E Y L S F T K K K G S V L L R

GTA GTC gac gac tac ctc ctc atc acc  
CAT CAG ctg ctg atg gag gag tag tgg

V V D D Y L L I T

<----- ctg ctg atg gag gag tag tgg  
a a a a a a a  
t t t t t  
C C  
Poly I

.....gac gat ttc ctc ttt ata aca..... <---Actual Genomic Sequence  
D D F L F I T

FIG. 58  
(CONTINUED)

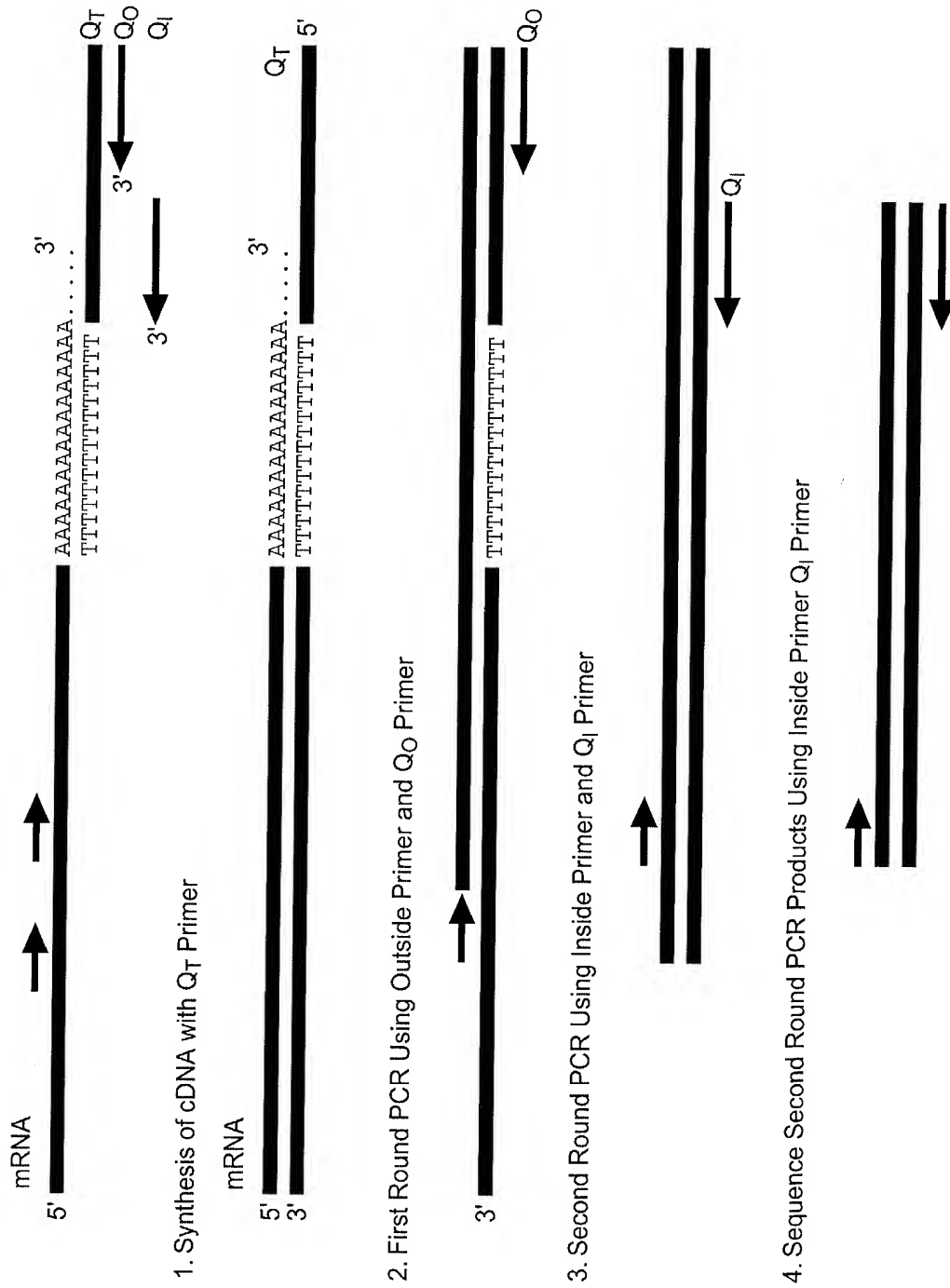


FIG. 59

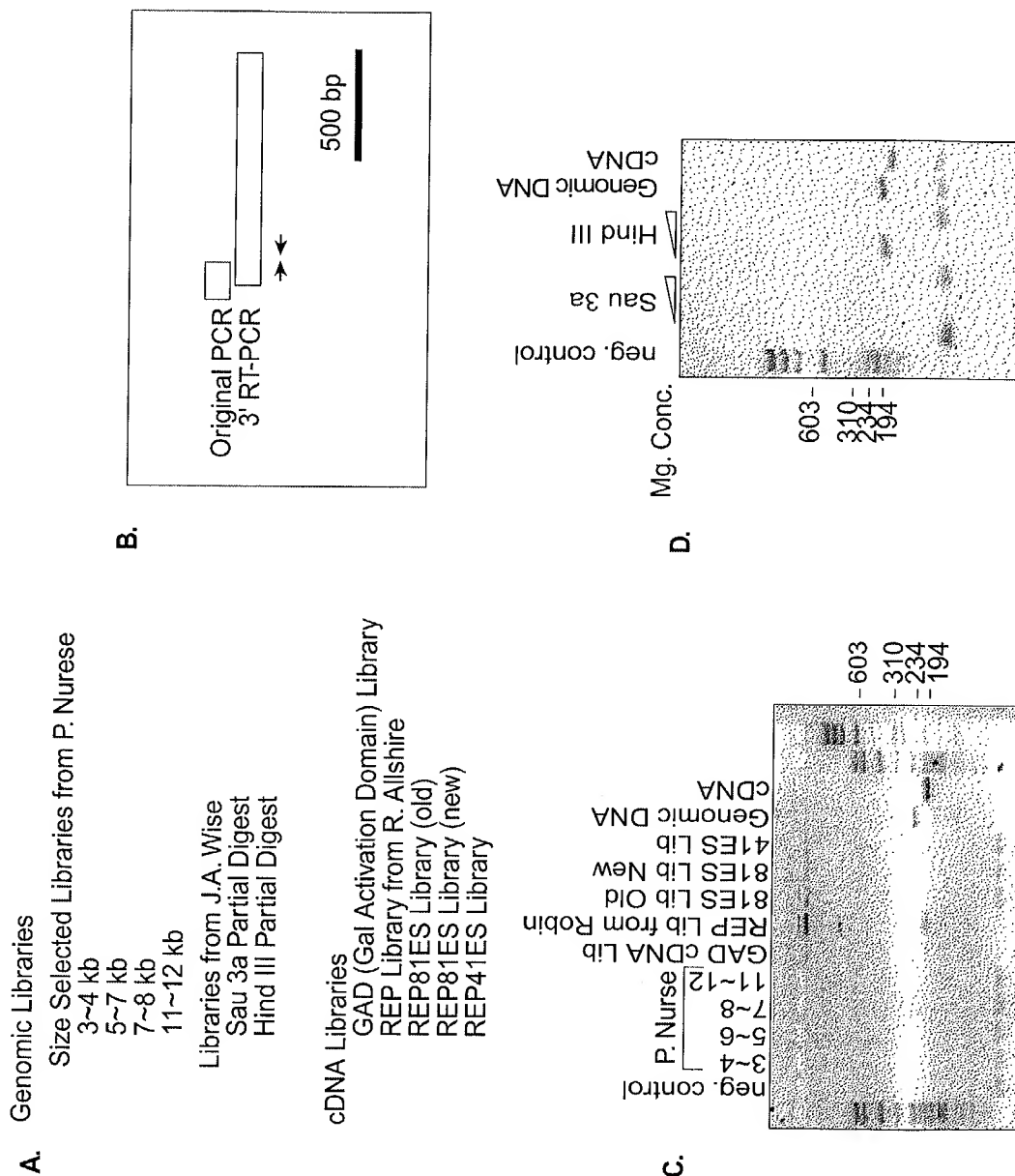
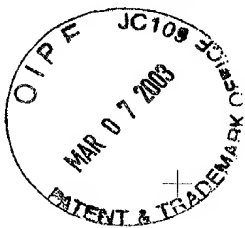


FIG. 60



65/103

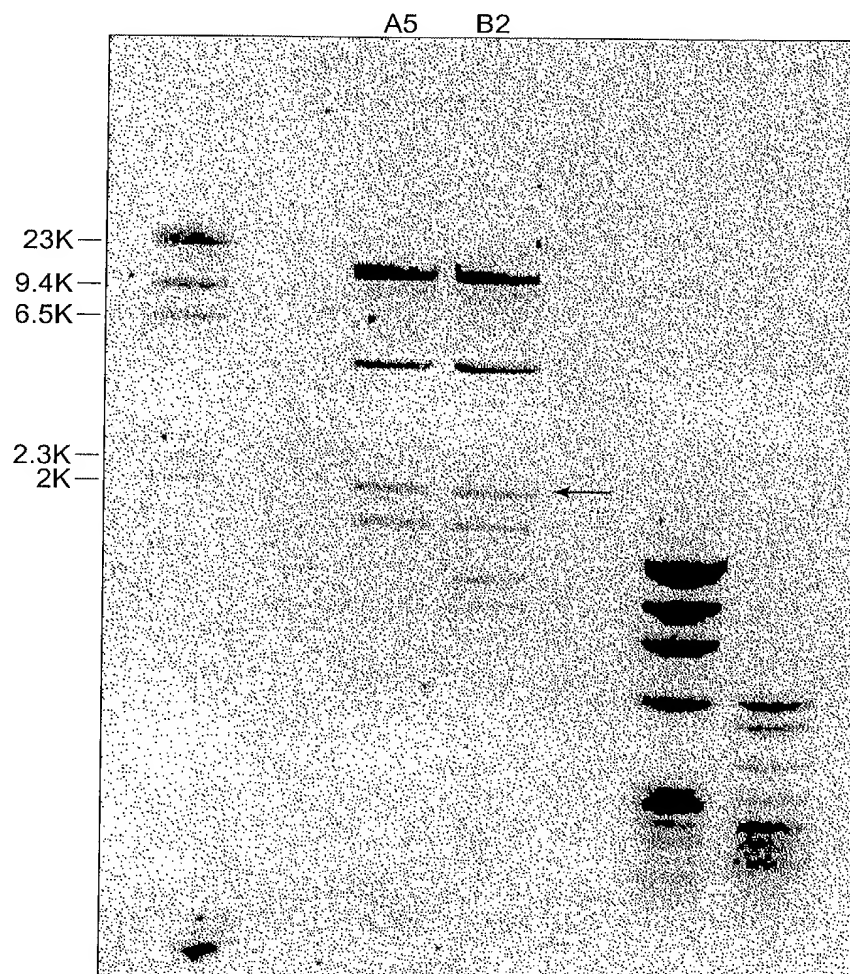
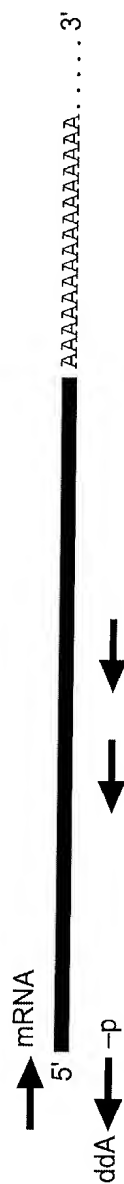


FIG. 61



1. Synthesis of cDNA with Specific Destination Primer



2. Ligate Oligo with 5' -P and blocked 3' to cDNA using T4 RNA Ligase



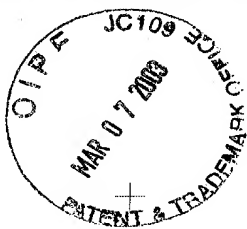
3. First Round PCR



4. Second Round PCR



FIG. 62



67/103

Motif O

S.p. Tez1p (429) . WLYNSFIPILOQFFYITESSDLNRRTVVYFRKDIW ... (35) ...  
S.c. Est2p (366) . WLFRLIPKIIQIFFYCTEISSTVT-IVYFRHDTW ... (35) ...  
E.a. p123 (441) . WIFEDLVVSLIRCFYVTEQQKSYKTYVYRKNIW ... (35) ...  
\* \*\*\* \*\* \* \* \* \*

Motif 1 Motif 2 K  
p hh h K hR h R  
AVIRLLPKK--NTFRLITN-LRKRF ... (61) ...  
S.p. Tez1p SKMRIIPKKSNNFRIIAPCRGAD ... (62) ...  
S.c. Est2p GKRLRIPKK--TTFRPIMTFNKKIV ... (61) ...  
E.a. p123 \* \*\*\* \*\* \* \*

Motif 3(A) AF  
h hDh GY h  
KKYFVRIDIKSCYDRIKQDLMFRIVK ... (89) ...  
S.p. Tez1p ELYFMKFDVKSCYDSIPRMECMRIK ... (75) ...  
S.c. Est2p KLFATMDIEKCYDSVNRKLSFLK ... (107) ...  
E.a. p123 \* \* \*\*\* \*

Motif 4(B')

hPQG pP hh h  
YLQKVGIPQGSILSSFLCHFYMEDLIDEVLSF ... (6) ...  
S.p. Tez1p YIREDLFGSSLSAPIVDLVYDDLIIFYSEF ... (8) ...  
S.c. Est2p YKQTKGIPQGLCVSSILSSFYATLEESSLGF ... (14) ...  
E.a. p123 \* \* \*\*\* \* \*

Y Motif 5(C)  
h F DDhhh  
VLLRVVDDFLFITVNNKDAKKFLNLSRGFEKHNFTSLEKTVINFENS . (205)  
S.p. Tez1p LILKLADDFLIISTDQQQVINIKKLAMGGFQKYNKARDKILAVSSQS . (173)  
S.c. Est2p LLMRLTDDYLLITTTQENNAVLFIKLIINVSRENGFKFNMKKIQTSFFPLS . (209)  
E.a. p123 \* \* \* \* \*

Motif 6(D)  
Gh h cK h

FIG. 63

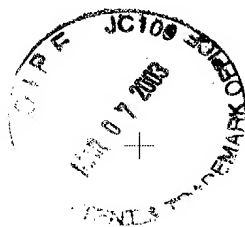


A.

Sp_Tip1p	1	- - - - -	MTEHHTPKSRILRFL	ENQYVYLCT	24
Sc_Est2p	1	- - - - -	- - - - -	MKILFEF	7
Ea_p123	1	MEVDVDNQADNHG	HSALKTCEEI	KEAKTL	33
Sp_Tip1p	25	LN	DYVQLVLRGSPA	SSY	57
Sc_Est2p	8	I	QDKLDIDLQTN	- - - - -	35
Ea_p123	34	I	QKVIRCRNQSQ	- - - - -	61
Sp_Tip1p	58	I	F	LHSTVVGFD	90
Sc_Est2p	36	E	IL	TTCFALPNSR	67
Ea_p123	62	I	VATPRDYNEED	FKVIARKEVF	94
Sp_Tip1p	91	V	VKQMFDE	SFERR	122
Sc_Est2p	68	C	I	IYLLTGELYN	93
Ea_p123	95	C	LVELLSS	SDVSDRQKLC	122
Sp_Tip1p	123	V	NG	VQNDLVST	155
Sc_Est2p	94	- - -	VNN	SLFCHSANVN	123
Ea_p123	123	- - -	LAKTHLLT	ALSTQKQYFF	152
Sp_Tip1p	156	S	D	AMHYLLSKGS	188
Sc_Est2p	124	T	YAFVDLLIN	YTVIQFN	155
Ea_p123	153	N	ELFRHL	YTKYLIFQRT	185
Sp_Tip1p	189	N	VFEET	VSKKRKRTIET	218
Sc_Est2p	156	H	LPPKWVQ	- - - - -	183
Ea_p123	186	L	KVNDKFDK	- KQKGGAA	217

FIG. 64



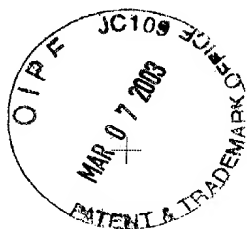


A.																																			
Sp_Tip1p	219	WNSISISRFSIFYRSSY	KFKQDL	YFN	LH	S	I	C	D	251																									
Sc_Est2p	184	N	-	-	-	-	-	-	-	200																									
Ea_p123	218	N	E	K	-	-	D	H	F	L	N	N	I	N	V	P	N	W	N	N	M	K	S	R	T	R	I	F	Y	C	T	H	E	N	248
Sp_Tip1p	252	R	N	T	V	H	M	W	L	Q	W	I	F	P	R	Q	F	G	L	I	N	A	F	Q	V	K	Q	L	H	K	V	I	P	L	284
Sc_Est2p	201	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	223	
Ea_p123	249	R	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	275	
Sp_Tip1p	285	V	S	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	313	
Sc_Est2p	224	T	N	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	252	
Ea_p123	276	F	T	N	I	F	R	F	N	R	I	R	K	K	L	K	D	K	V	I	E	K	I	A	Y	M	L	E	K	V	K	D	F	N	308
Sp_Tip1p	314	L	S	K	V	N	H	Y	C	P	Y	I	D	-	T	H	D	D	E	K	I	L	S	Y	S	L	K	P	N	Q	-	-	-	-	342
Sc_Est2p	253	Y	V	S	I	L	N	S	I	C	P	P	L	E	G	T	V	L	D	L	S	H	L	S	R	Q	S	P	K	E	R	-	-	-	282
Ea_p123	309	F	N	Y	Y	L	T	K	S	C	P	L	P	E	N	W	R	E	R	K	Q	K	I	E	N	L	I	N	K	T	R	E	E	K	341
Sp_Tip1p	343	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	359	
Sc_Est2p	283	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	299	
Ea_p123	342	S	K	Y	Y	E	E	L	F	S	Y	T	T	D	N	K	C	V	T	Q	F	I	N	E	F	F	Y	N	I	L	P	K	D	F	374
Sp_Tip1p	360	W	G	N	Q	R	I	F	E	I	I	L	K	D	L	E	T	F	L	K	L	S	R	Y	E	S	F	S	L	H	Y	L	M	S	392
Sc_Est2p	300	F	G	S	K	K	N	K	G	K	I	I	K	N	L	N	L	L	S	L	P	L	N	G	Y	L	P	F	D	S	L	L	K	332	
Ea_p123	375	L	T	G	-	R	N	R	K	N	F	Q	K	V	K	K	Y	V	E	L	N	K	H	E	L	I	H	K	N	L	L	E	406		
Sp_Tip1p	393	N	I	K	I	S	E	I	E	W	L	V	L	G	K	R	S	N	A	K	M	C	L	S	D	F	E	K	R	K	I	F	A	425	
Sc_Est2p	333	K	L	R	L	K	D	F	R	W	L	F	I	S	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	362
Ea_p123	407	K	I	N	T	R	E	I	S	W	M	Q	V	E	T	S	-	A	K	H	F	Y	Y	F	D	H	E	N	-	I	Y	V	L	W	437

FIG. 64  
(CONTINUED)

A.	Sp_Tip1p	426	E	F	I	Y	W	L	Y	N	S	F	I	I	P	I	L	Q	S	F	F	Y	I	T	E	S	S	D	L	R	N	R	T	V	Y	458
	Sc_Est2p	363	C	F	I	S	W	L	F	R	Q	L	I	P	K	I	I	Q	T	F	F	Y	C	T	E	I	S	S	T	V	T	-	I	V	Y	394
	Ea_p123	438	K	L	L	R	W	I	F	E	D	L	V	V	S	L	I	R	C	F	F	Y	V	T	E	Q	Q	K	S	Y	S	K	T	Y	Y	470
	Sp_Tip1p	459	F	R	K	D	I	W	K	L	L	C	R	P	F	I	T	S	M	K	M	E	A	F	E	K	I	N	E	N	N	V	R	M	D	491
	Sc_Est2p	395	F	R	H	D	T	W	N	K	L	I	T	P	F	I	V	E	Y	F	K	T	Y	L	V	E	N	N	V	C	R	N	H	N	S	427
	Ea_p123	471	Y	R	K	N	I	W	D	V	I	M	K	M	S	I	A	D	L	K	K	E	T	L	A	E	V	Q	E	K	E	V	E	E	W	503
	Sp_Tip1p	492	T	Q	K	T	T	L	P	A	V	I	R	L	L	P	K	K	-	-	N	T	F	R	L	I	T	N	L	R	K	R	F	L	522	
	Sc_Est2p	428	Y	T	L	S	N	F	N	H	S	K	M	R	I	I	P	K	K	S	N	N	E	F	R	I	I	A	I	P	C	R	G	A	D	460
	Ea_p123	504	K	K	S	L	G	F	A	P	G	K	L	R	L	I	P	K	K	-	-	T	T	F	R	P	I	M	T	F	N	K	I	V	534	
	Sp_Tip1p	523	I	K	M	G	S	N	K	K	M	L	V	S	T	N	Q	T	L	R	P	V	A	S	I	L	K	H	L	I	N	E	-	-	-	552
	Sc_Est2p	461	E	E	E	-	-	F	T	I	Y	K	E	N	H	K	N	A	I	Q	P	T	Q	K	I	L	E	Y	L	R	N	K	R	P	T	491
	Ea_p123	535	N	S	D	-	-	R	K	T	T	K	L	T	T	N	T	K	L	L	N	S	H	L	M	L	K	T	L	K	N	R	-	M	F	564
	Sp_Tip1p	553	E	S	S	G	I	P	F	N	L	E	V	Y	M	K	L	L	T	F	K	K	D	L	L	K	H	R	M	F	G	R	-	K	K	584
	Sc_Est2p	492	S	F	T	K	I	Y	S	P	T	Q	I	A	D	R	I	K	E	F	K	Q	R	L	L	K	K	F	N	N	V	L	P	E	L	524
	Ea_p123	565	K	D	P	F	G	F	A	V	F	N	Y	D	V	M	K	K	Y	E	E	F	V	C	K	W	K	Q	V	G	Q	P	K	L	597	
	Sp_Tip1p	585	Y	F	V	R	I	D	I	K	S	C	Y	D	R	I	K	Q	D	L	M	F	R	I	V	K	K	K	L	K	D	P	E	-	F	616
	Sc_Est2p	525	Y	F	M	K	F	D	V	K	S	C	Y	D	S	I	P	R	M	E	C	M	R	I	L	K	D	A	L	K	N	E	N	G	F	557
	Ea_p123	598	F	F	A	T	M	D	I	E	K	C	Y	D	S	V	N	R	E	K	L	S	T	F	L	K	T	T	K	L	L	S	S	D	F	630
	Sp_Tip1p	617	V	I	R	K	Y	A	T	I	H	A	T	S	D	R	A	T	K	N	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	634
	Sc_Est2p	558	F	V	R	S	Q	Y	F	F	N	T	N	T	G	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	570
	Ea_p123	631	W	I	M	T	A	Q	I	L	K	R	K	N	I	V	I	D	S	K	N	F	R	K	K	E	M	K	D	Y	F	R	Q	K	663	

FIG. 64  
(CONTINUED)



71/103

A.

Sp_Tip1p	635	F	V	S	E	A	F	S	Y	F	D	M	V	P	F	E	K	V	V	Q	L	L	S	-	-	M	K	T	S	D	T	L	F	V	665	
Sc_Est2p	571	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	591	
Ea_p123	664	F	Q	K	I	A	L	E	G	G	Q	Y	P	T	L	F	S	V	L	E	N	E	Q	N	D	L	N	A	K	K	T	L	I	V	696	
Sp_Tip1p	666	D	F	V	D	Y	W	T	K	S	S	S	E	I	F	K	M	L	K	E	H	L	S	G	H	I	V	K	I	G	N	S	Q	Y	698	
Sc_Est2p	592	D	N	V	R	T	V	H	L	S	N	Q	D	V	I	N	V	V	E	M	E	I	F	K	T	A	L	W	V	E	D	K	C	Y	624	
Ea_p123	697	E	A	K	Q	R	N	Y	F	K	K	D	N	L	L	Q	P	V	I	N	I	C	Q	Y	N	Y	I	N	F	N	G	K	F	Y	729	
Sp_Tip1p	699	L	Q	K	V	G	I	P	Q	G	S	I	L	S	S	F	L	C	H	F	Y	M	E	D	L	I	D	E	Y	L	S	F	T	K	731	
Sc_Est2p	625	I	R	E	D	G	L	F	Q	G	S	S	L	S	A	P	I	V	D	L	V	Y	D	D	L	L	E	F	Y	S	E	F	K	A	657	
Ea_p123	730	K	Q	T	K	G	I	P	Q	G	L	C	V	S	S	I	L	S	S	F	Y	A	T	L	E	E	S	S	L	G	F	L	R	762		
Sp_Tip1p	732	K	K	G	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	756		
Sc_Est2p	658	S	P	S	Q	D	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	684		
Ea_p123	763	D	E	S	M	N	P	E	N	P	N	V	N	L	L	M	R	L	T	D	D	Y	L	L	I	T	T	Q	E	N	N	A	V	L	795	
Sp_Tip1p	757	F	L	N	L	S	L	R	G	F	E	K	H	N	F	S	T	S	L	E	K	T	V	I	N	F	E	N	S	N	G	-	-	-	-	786
Sc_Est2p	685	I	K	K	L	A	M	G	G	F	Q	K	Y	N	A	K	A	N	R	D	K	I	L	A	V	S	S	Q	S	D	-	-	-	-	-	713
Ea_p123	796	F	I	E	K	L	I	N	V	S	R	E	N	G	F	K	F	N	M	K	L	Q	T	S	F	P	L	S	P	S	K	F	A	828		
Sp_Tip1p	787	-	-	-	I	I	N	N	T	F	F	N	E	S	K	K	R	M	P	F	F	G	F	S	V	N	M	R	S	L	D	T	L	L	816	
Sc_Est2p	714	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	739		
Ea_p123	829	K	Y	G	M	D	S	V	E	E	Q	N	I	V	Q	D	Y	C	D	W	I	G	I	S	I	D	M	K	T	L	A	L	M	P	861	
Sp_Tip1p	817	A	C	P	K	I	D	E	A	L	F	N	S	T	S	V	E	L	T	K	H	M	G	K	S	F	F	Y	K	I	L	R	S	S	849	
Sc_Est2p	740	N	N	F	H	I	R	S	K	S	S	K	G	I	F	R	S	L	I	A	L	F	N	T	R	I	S	Y	K	T	I	D	T	N	772	
Ea_p123	862	N	I	N	L	R	I	E	G	I	L	C	T	L	N	L	N	M	Q	T	K	K	A	S	M	W	L	K	K	L	K	S	F	894		

FIG. 64  
(CONTINUED)



72/103

A.

Sp_Tip1p	850	L	A	S	F	A	Q	V	F	I	D	I	T	H	N	S	K	F	N	S	C	C	N	I	Y	R	L	G	Y	S	M	C	M	R	882	
Sc_Est2p	773	L	N	S	T	N	T	V	L	M	Q	I	D	H	V	V	K	N	I	S	E	C	-	-	-	-	-	-	-	-	-	-	-	-	-	793
Ea_p123	895	L	M	N	I	T	H	Y	F	R	K	T	I	T	T	E	D	F	A	N	K	T	L	N	K	L	F	I	S	G	G	Y	K	927		
Sp_Tip1p	883	A	Q	A	Y	L	K	R	M	K	D	I	F	I	P	Q	R	M	F	I	T	D	L	L	N	V	I	G	R	K	I	W	K	K	915	
Sc_Est2p	794	-	-	-	Y	K	S	A	F	K	D	L	S	I	N	-	-	V	T	Q	N	M	Q	F	H	S	F	L	Q	R	I	I	E	M	821	
Ea_p123	928	Y	M	Q	C	A	K	E	Y	K	D	H	F	K	K	N	L	A	M	S	S	M	I	D	L	E	V	S	K	I	I	Y	S	V	960	
Sp_Tip1p	916	L	A	E	I	L	G	Y	T	S	R	R	F	L	S	S	A	E	V	K	W	L	F	C	L	G	M	R	D	G	L	K	P	S	948	
Sc_Est2p	822	T	V	S	G	C	P	I	T	K	C	D	P	L	I	E	Y	E	V	R	F	T	I	L	N	G	F	L	E	S	L	S	S	N	854	
Ea_p123	961	T	R	A	F	F	K	Y	L	V	C	N	I	K	D	T	I	F	G	E	E	H	Y	P	D	F	F	L	S	T	L	K	H	F	993	
Sp_Tip1p	949	F	K	Y	H	P	C	F	E	Q	L	I	Y	Q	F	Q	S	L	T	D	L	I	K	P	L	R	P	V	L	R	Q	V	L	F	981	
Sc_Est2p	855	T	S	-	-	-	-	-	-	-	-	-	-	-	-	K	F	K	D	N	I	I	L	L	R	K	E	I	Q	H	L	Q	A	Y	I	877
Ea_p123	994	I	E	I	F	S	-	-	-	-	-	-	-	-	-	T	K	K	Y	I	F	N	R	V	C	M	I	L	K	A	K	E	A	K	L	1023
Sp_Tip1p	982	L	H	R	R	I	A	D	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	988		
Sc_Est2p	878	I	Y	I	H	I	V	N	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	884		
Ea_p123	1024	Q	S	L	I	Q	Y	D	A	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1031		

FIG. 64  
(CONTINUED)

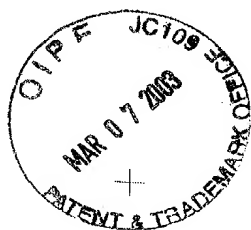


73/103

B.

Sp_Tip1p	1	- - - - -	MTEHHTPKSRILRFL	ENQYVYLCT	24
Sc_Est2p	1	- - - - -	- - - - -	MKILFEF	7
Ea_p123	1	MEVDVDNQADNHG	HSALKTCEEI	KEAKTLYSW	33
Sp_Tip1p	25	LNDYVQLVLRGSPA	SSY	SNICERLRSDVQTSFS	57
Sc_Est2p	8	IQDKLDIDLQTN	- - - - -	ENLKCGHFNGLD	35
Ea_p123	34	IQKVIRCRNQSQ	- - - - -	DLEDIKIFAQTN	61
Sp_Tip1p	58	IFLHSTVVGFD	SKPD	EGVQFSSPKCSQSELI	90
Sc_Est2p	36	EILTTTCFALPNSR	- - - - -	KIALPCLPGDLSHKAVI	67
Ea_p123	62	I VATPRDYNEED	FKVI	ARKEVFSTGLMIELI	94
Sp_Tip1p	91	VVKQMFDESFERR	- - - - -	NLLMKGF	122
Sc_Est2p	68	CIYLLTGELYN	- - - - -	NVLTFGYK	93
Ea_p123	95	CLVELLSSSDVSDRQ	KLQCFG	FQLKGNQ	122
Sp_Tip1p	123	VNGVQNDLVSTFP	NYLISILESKN	WQLLEIIG	155
Sc_Est2p	94	- - - - -	VNNSLFCHSANVN	VTLLKGAAWKMFHSLVG	123
Ea_p123	123	- - - - -	LAKTHLLTALSTQKQ	YFFQDEWNQVVRAMIG	152
Sp_Tip1p	156	SDAMHY	LLSKGSI	FEALPNDNYLQ	188
Sc_Est2p	124	TYAFVD	LLIN	YTVIQFN - GQFF	155
Ea_p123	153	NELFRHL	YTKYL	IFQRTSEGT	185
Sp_Tip1p	189	NVFEETVSKKRKR	TIET	SITQN - - - -	218
Sc_Est2p	156	HLPPKWVQ	- - - - -	RSSSSSATAAQI	183
Ea_p123	186	LKVNDKFDK	- - - - -	KQKGGGAADMNEPRCCSTCKYNVK	217

FIG. 64  
(CONTINUED)



B.

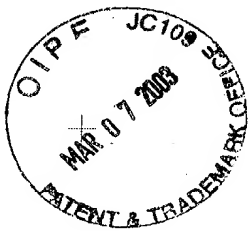
Sp_Tip1p	219	WNSISISRFSIFYRSSYKKFKQDL	YFNLHSICD	251				
Sc_Est2p	184	N-----	--KQFLHKLNNINSSFFFP	200				
Ea_p123	218	NEK--DHFLNNINVPNWNMMKSRTRI	FYCTHFN	248				
Sp_Tip1p	252	RNTVHMWLQWIFPRQFGLINAFQVKQL	HKV IPL	284				
Sc_Est2p	201	--YSKILPSS--	--SIKKLTDLREAI	223				
Ea_p123	249	R-----NNQFFKKHEFVSNKNNI	SAMDRAQTI	275				
Sp_Tip1p	285	VS-----QSTVVPKRLLKVVYPLI	EQTAKRLHRI	313				
Sc_Est2p	224	TN-----LVKIPQRLKVRINLT	LQKLLKRHKRLN	262				
Ea_p123	276	FTNIFRFNRIRKKLKDKVIEKIA	YMLEKVKDFN	308				
Sp_Tip1p	314	LSKVYNHYCPYID-THDDEKIL	SYSLKPNQ--	342				
Sc_Est2p	253	YVSI LNSICP	LEGTVLDLSHL	SRQSPKER--	282			
Ea_p123	309	FNYYLT	KSCPLPENWRERKQKIEN	LINKTREEK	341			
Sp_Tip1p	343	-----	VFAFLRSILVRVFPKLI	359				
Sc_Est2p	283	-----	VLFKFIIVILQKLLPQEM	299				
Ea_p123	342	SKYYEELFSYTTDNKCV	TTQFIN	EFFYNILPKDF	374			
Sp_Tip1p	360	WGNQRI	FEIILK	DLETF	LKLSRYESFSLHYL	MS	392	
Sc_Est2p	300	FGSKKNKGKII	KNLNL	LSLPL	NGYLP	FDSSL	LK	332
Ea_p123	375	LTG-RNRKNFQ	KVKKY	VEL	NKHEL	IHKNN	LE	406
Sp_Tip1p	393	NIKISEI	EWLVLGKR	SN	AKMCL	SDFE	EKRKQIFA	425
Sc_Est2p	333	KLRLKDFR	WLFI	S--DI	WFTKHNF	ENLNQ	LAI	362
Ea_p123	407	KINTREI	SWMQVETS	-AKH	FYYFDH	EN-I	YVLW	437

FIG. 64  
(CONTINUED)

B.

Sp_Tip1p	426	EF I YW L Y N S F I I P I L Q S F F Y I T E S S D L R N R T V Y	458
Sc_Est2p	363	C F I S W L F R Q L I P K I I Q T F F Y C T E I S S T V T - I V Y	394
Ea_p123	438	K L L R W I F E D L V V S L I R C F F Y V T E Q Q K S Y S K T Y Y	470
Sp_Tip1p	459	F R K D I W K L L C R P F I T S M K M E A F E K I N E N N V R M D	491
Sc_Est2p	395	F R H D T W N K L I T P F I V E Y F K T Y L V E N N V C R N H N S	427
Ea_p123	471	Y R K N I W D V I M K M S I A D L K K E T L A E V Q E K E V E E W	503
Sp_Tip1p	492	T Q K T T L P P A V I R L L P K K - - N T F R L I T N L R K R F L	522
Sc_Est2p	428	Y T L S N F N H S K M R I I P K K S N N E F R I I A I P C R G A D	460
Ea_p123	504	K K S L G F A P G K L R I P K K - - T T F R P I M T F N K K I V	534
Sp_Tip1p	523	I K M G S N K K M L V S T N Q T L R P V A S I L K H L I N E - - -	552
Sc_Est2p	461	E E E - - F T I Y K E N H K N A I Q P T Q K I L E Y L R N K R P T	491
Ea_p123	535	N S D - - R K T T K L T T N T K L L N S H L M L K T L K N R - M F	564
Sp_Tip1p	553	E S S G I P F N L E V Y M K L L T F K K D L L K H R M F G R - K K	584
Sc_Est2p	492	S F T K I Y S P T Q I A D R I K E F K Q R L L K K F N N V L P E L	524
Ea_p123	565	K D P F G F A V F N Y D D V M K K Y E E F V C K W K Q V G Q P K L	597
Sp_Tip1p	585	Y F V R I D I K S C Y D R I K Q D L M F R I V K K K L K D P E - F	616
Sc_Est2p	525	Y F M K F D V K S C Y D S I P R M E C M R I L K D A L K N E N G F	557
Ea_p123	598	F F A T M D I E K C Y D S V N R E K L S T F L K T T K L L S S D F	630
Sp_Tip1p	617	V I R K Y A T I H A T S D R A T K N - - - - -	634
Sc_Est2p	558	F V R S Q Y F F N T N T G - - - - -	570
Ea_p123	631	W I M T A Q I L K R K N N I V I D S K N F R K K E M K D Y F R Q K	663

FIG. 64  
(CONTINUED)



76/103

B.

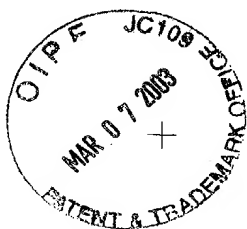
Sp_Tip1p	635	FVSEAFSYFDMVPF	EK	V	V	Q	L	L	S	-	-	M	K	T	S	D	T	L	F	V	665															
Sc_Est2p	571	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	591															
Ea_p123	664	FQK	I	A	L	E	G	G	Q	Y	P	T	L	F	S	V	L	E	N	E	Q	N	D	L	N	A	K	K	T	L	I	V	696			
Sp_Tip1p	666	D	F	V	D	Y	W	T	K	S	S	S	E	I	F	K	M	L	K	E	H	L	S	G	H	I	V	K	I	G	N	S	Q	Y	698	
Sc_Est2p	592	D	N	V	R	T	V	H	L	S	N	Q	D	V	I	N	V	V	E	M	E	I	F	K	T	A	L	W	V	E	D	K	C	Y	624	
Ea_p123	697	E	A	K	Q	R	N	Y	F	K	K	D	N	L	Q	P	V	I	N	I	C	Q	N	Y	I	N	F	N	G	K	F	Y		729		
Sp_Tip1p	699	L	Q	K	V	G	I	P	Q	G	S	I	L	S	S	F	L	C	H	F	Y	M	E	D	L	I	D	E	Y	L	S	F	T	K	731	
Sc_Est2p	625	I	R	E	D	G	L	F	Q	G	S	S	L	S	A	P	I	V	D	L	V	Y	D	D	L	L	E	F	Y	S	E	F	F	K	A	657
Ea_p123	730	K	Q	T	K	G	I	P	Q	G	L	C	V	S	S	I	L	S	S	F	Y	A	T	L	L	E	E	S	S	L	G	F	L	R	762	
Sp_Tip1p	732	K	K	G	-	-	-	-	-	-	-	-	-	-	S	V	L	L	R	V	V	D	D	F	L	F	I	T	V	N	K	K	D	A	K	756
Sc_Est2p	658	S	P	S	Q	D	-	-	-	-	-	-	-	-	T	L	I	L	K	L	A	D	D	F	L	I	I	S	T	D	Q	Q	V	I	N	684
Ea_p123	763	D	E	S	M	N	P	E	N	P	N	V	N	L	L	M	R	L	T	D	D	Y	L	L	I	T	T	Q	E	N	N	A	V	L		795
Sp_Tip1p	757	F	L	N	L	S	L	R	G	F	E	K	H	N	F	S	T	S	L	E	K	T	V	I	N	F	E	N	S	N	G	-	-	-		786
Sc_Est2p	685	I	K	K	L	A	M	G	G	F	Q	K	Y	N	A	K	A	N	R	D	K	I	L	A	V	S	S	Q	S	D	-	-	-	-		713
Ea_p123	796	F	I	E	K	L	I	N	V	S	R	E	N	G	F	K	F	N	M	K	K	L	Q	T	S	F	P	L	S	P	S	K	F	A		828
Sp_Tip1p	787	-	-	-	I	I	N	N	T	F	F	N	E	S	K	K	R	M	P	F	F	G	F	S	V	N	M	R	S	L	D	T	L	L		816
Sc_Est2p	714	-	-	-	-	-	-	-	-	-	-	-	-	-	M	H	I	F	V	K	E	L	E	V	W	K	H	S	S	T	M				739	
Ea_p123	829	K	Y	G	M	D	S	V	E	E	Q	N	I	V	Q	D	Y	C	D	W	I	G	I	S	I	D	M	K	T	L	A	L	M	P		861
Sp_Tip1p	817	A	C	P	K	I	D	E	A	L	F	N	S	T	S	V	E	L	T	K	H	M	G	K	S	F	F	Y	K	I	L	R	S	S		849
Sc_Est2p	740	N	N	F	H	I	R	S	K	S	S	K	G	I	F	R	S	L	I	A	L	F	N	T	R	I	S	Y	K	T	I	D	T	N		772
Ea_p123	862	N	I	N	L	R	I	E	G	I	L	C	T	L	N	L	N	M	Q	T	K	K	A	S	M	W	L	K	K	K	L	K	S	F		894

FIG. 64  
(CONTINUED)

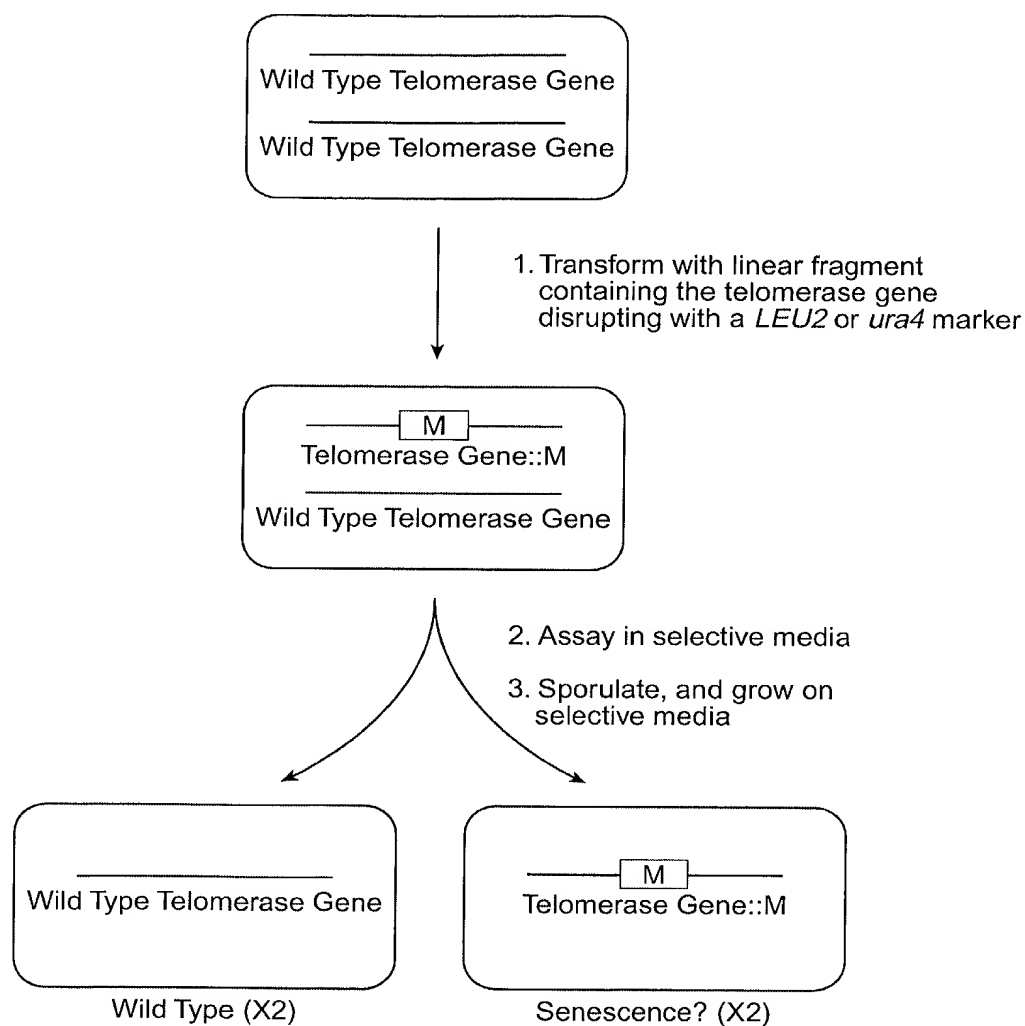


B.			
Sp_Tip1p	850	L A S F A Q V F I D I T H N S K F N S C C N I Y R L G Y S M C M R	882
Sc_Est2p	773	L N S T N T V L M Q I D H V V K N I S E C - - - - - - - - - -	793
Ea_p123	895	L M N N I T H Y F R K T I T T E D F A N K T L N K L F I S G G Y K	927
Sp_Tip1p	883	A Q A Y L K R M K D I F I P Q R M F I T D L L N V I G R K I I W K K	915
Sc_Est2p	794	- - - Y K S A F K D L S I N - - V T Q N M Q F H S F L Q R I I E M	821
Ea_p123	928	Y M Q C A K E Y K D H F K K N L A M S S M I D L E V S K I I Y S V	960
Sp_Tip1p	916	L A E I L G Y T S R R F L S S A E V K W L F C L G M R D G L K P S	948
Sc_Est2p	822	T V S G C P I T K C D P L I E Y E V R F T I L N G F L E S L S S N	854
Ea_p123	961	T R A F F K Y L V C N I K D T I F G E E H Y P D F F L S T L K H F	993
Sp_Tip1p	949	F K Y H P C F E Q L I Y Q F Q S L T D L I K P L R P V L R Q V L F	981
Sc_Est2p	855	T S - - - - - - - - - K F F K D N I I L L R K E I Q H L Q A Y I Y	877
Ea_p123	994	I E I F S - - - T K K Y I F N R V C M I L K A K E A K L K S D Q C	1023
Sp_Tip1p	982	L H R R I A D -	988
Sc_Est2p	878	I Y I H I V N -	884
Ea_p123	1024	Q S L I Q Y D A	1031

FIG. 64  
(CONTINUED)



78/103



(These cells will show a senescence phenotype if the disrupted gene encodes a telomerase subunit.)

FIG. 65

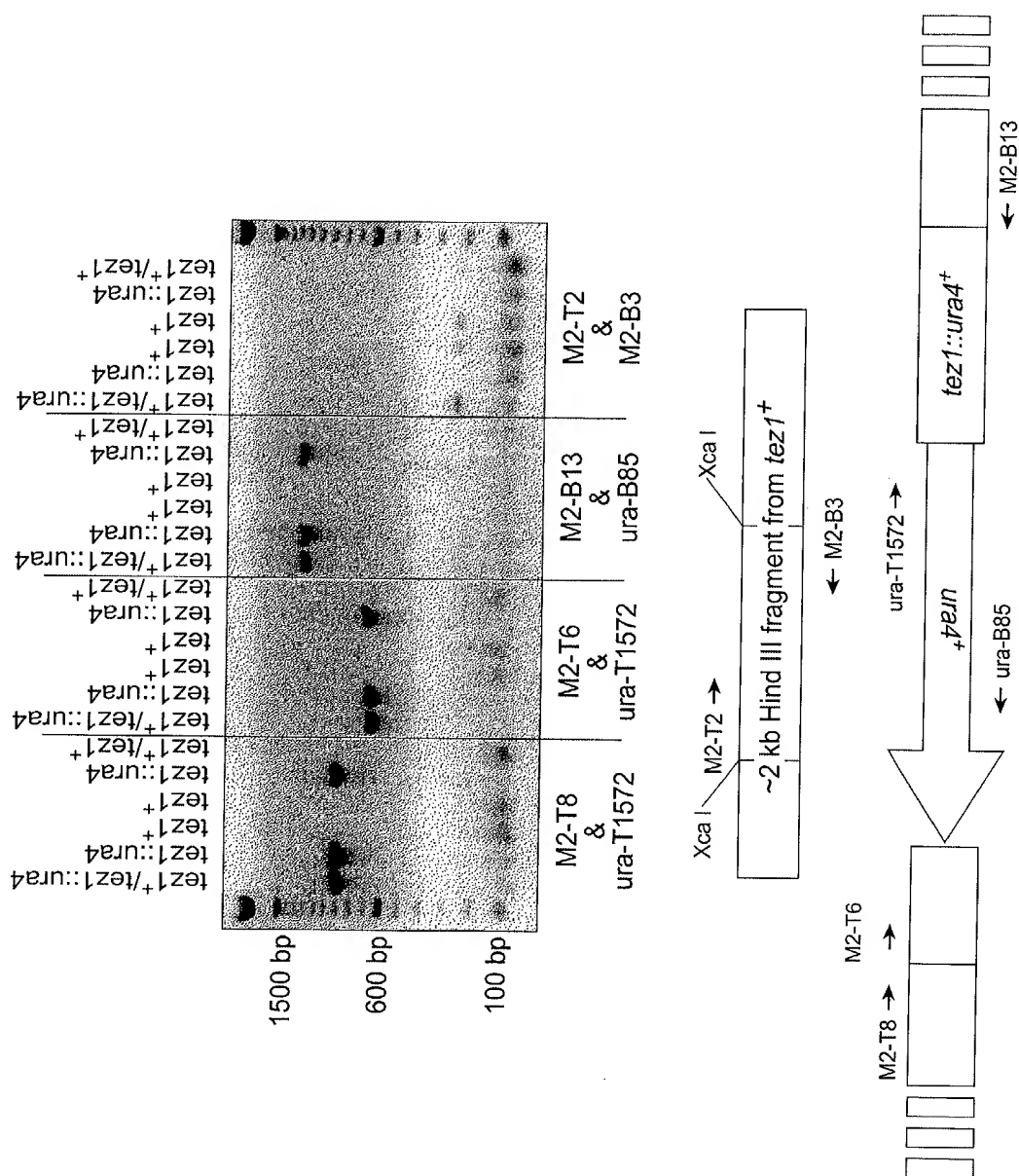


FIG. 64

80/103

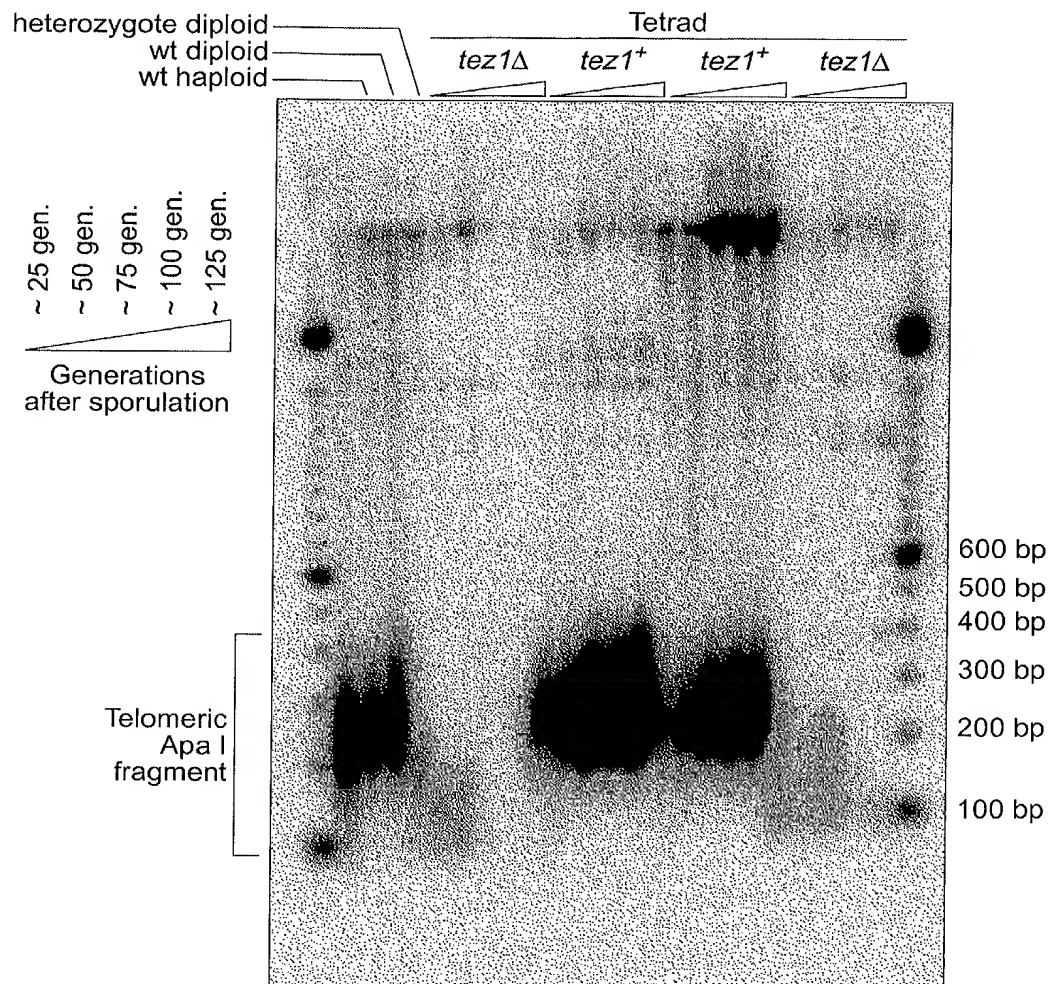
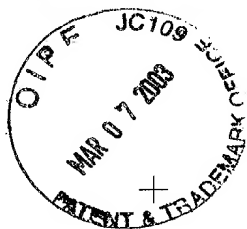


FIG. 67



81/103

1  
GCCAAGTTCCTGCACTGGCTG met ser val tyr val val glu leu leu  
ATG AGT GTG TAC GTC GTC GAG CTG CTC

10 20  
arg ser phe phe tyr val thr glu thr thr phe gln lys asn arg  
AGG TCT TTC TTT TAT GTC ACG GAG ACC ACG TTT CAA AAG AAC AGG

30  
leu phe phe tyr arg lys ser val trp ser lys leu gln ser ile  
CTC TTT TTC TAC CGG AAG AGT GTC TGG AGC AAG TTG CAA AGC ATT

40 50  
gly ile arg gln his leu lys arg val gln leu arg glu leu ser  
GGA ATC AGA CAG CAC TTG AAG AGG GTG CAG CTG CGG GAG CTG TCG

60  
glu ala glu val arg gln his arg glu ala arg pro ala leu leu  
GAA GCA GAG GTC AGG CAG CAT CGG GAA GCC AGG CCC GCC CTG CTG

70 80  
thr ser arg leu arg phe ile pro lys pro asp gly leu arg pro  
ACG TCC AGA CTC CGC TTC ATC CCC AAG CCT GAC GGG CTG CGG CCG

90  
ile val asn met asp tyr val val gly ala arg thr phe arg arg  
ATT GTG AAC ATG GAC TAC GTC GTG GGA GCC AGA ACG TTC CGC AGA

100 110  
glu lys ala glu arg leu thr ser arg val lys ala leu phe  
GAA AAG ARG GCC GAG CGT CTC ACC TCG AGG GTG AAG GCA CTG TTC

120  
ser val leu asn tyr glu arg ala arg arg pro gly leu leu gly  
AGC GTG CTC AAC TAC GAG CGG GCG CGG CGC CCC GGC CTC CTG GGC

130 140  
ala ser val leu gly leu asp asp ile his arg ala trp arg thr  
GCC TCT GTG CTG GGC CTG GAC GAT ATC CAC AGG GCC TGG CGC ACC

150  
phe val leu arg val arg ala gln asp pro pro pro glu leu tyr  
TTC GTG CTG CGT GTG CGG GCC CAG GAC CCG CCG CCT GAG CTG TAC

160 170  
phe val lys val asp val thr gly ala tyr asp thr ile pro gln  
TTT GTC AAG GTG GAT GTG ACG GGC GCG TAC GAC ACC ATC CCC CAG

180  
asp arg leu thr glu val ile ala ser ile ile lys pro gln asn  
GAC AGG CTC ACG GAG GTC ATC GCC AGC ATC ATC AAA CCC CAG AAC

190 200  
thr tyr cys val arg arg tyr ala val val gln lys ala ala met  
ACG TAC TGC GTG CGT CGG TAT GCC GTG GTC CAG AAG GCC GCC ATG

FIG. 68

+



82/103

210  
gly thr ser ala arg pro ser arg ala thr ser tyr val gln cys  
GGC ACG TCC GCA AGG CCT TCA AGA GCC ACG TCC TAC GTC CAG TGC

220 230  
gln gly ile pro gln gly ser ile leu ser thr leu leu cys ser  
CAG GGG ATC CCG CAG GGC TCC ATC CTC TCC ACG CTG CTC TGC AGC

240  
leu cys tyr gly asp met glu asn lys leu phe ala gly ile arg  
CTG TGC TAC GGC GAC ATG GAG AAC AAG CTG TTT GCG GGG ATT CGG

250 260  
arg asp gly leu leu leu arg leu val asp asp phe leu leu val  
CGG GAC GGG CTG CTC CTG CGT TTG GTG GAT GAT TTC TTG TTG GTG

270  
thr pro his leu thr his ala lys thr phe leu arg thr leu val  
ACA CCT CAC CTC ACC CAC GCG AAA ACC TTC CTC AGG ACC CTG GTC

280 290  
arg gly val pro glu tyr gly cys val val asn leu arg lys thr  
CGA GGT GTC CCT GAG TAT GGC TGC GTG GTG AAC TTG CGG AAG ACA

300  
val val asn phe pro val glu asp glu ala leu gly gly thr ala  
GTG GTG AAC TTC CCT GTA GAA GAC GAG GCC CTG GGT GGC ACG GCT

310 320  
phe val gln met pro ala his gly leu phe pro trp cys gly leu  
TTT GTT CAG ATG CCG GCC CAC GGC CTA TTC CCC TGG TGC GGC CTG

330  
leu leu asp thr arg thr leu glu val gln ser asp tyr ser ser  
CTG CTG GAT ACC CGG ACC CTG GAG GTG CAG AGC GAC TAC TCC AGC

340 350  
tyr ala arg thr ser ile arg ala ser leu thr phe asn arg gly  
TAT GCC CGG ACC TCC ATC AGA GCC AGT CTC ACC TTC AAC CGC GGC

360  
phe lys ala gly arg asn met arg arg lys leu phe gly val leu  
TTC AAG GCT GGG AGG AAC ATG CGT CGC AAA CTC TTT GGG GTC TTG

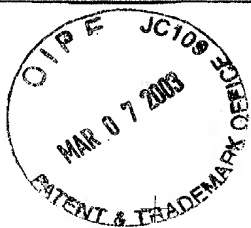
370 380  
arg leu lys cys his ser leu phe leu asp leu gln val asn ser  
CGG CTG AAG TGT CAC AGC CTG TTT CTG GAT TTG CAG GTG AAC AGC

390  
leu gln thr val cys thr asn ile tyr lys ile leu leu leu gln  
CTC CAG ACG GTG TGC ACC AAC ATC TAC AAG ATC CTC CTG CTG CAG

400 410  
ala tyr arg phe his ala cys val leu gln leu pro phe his gln  
GCG TAC AGG TTT CAC GCA TGT GTG CTG CAG CTC CCA TTT CAT CAG

FIG. 68  
(CONTINUED)

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83/103

420  
gln val trp lys asn pro his phe ser cys ala ser ser leu thr  
CAA GTT TGG AAG AAC CCA CAT TTT TCC TGC GCG TCA TCT CTG ACA

430 440  
arg leu pro leu leu leu his pro glu ser gln glu arg arg asp  
CGG CTC CCT CTG CTA CTC CAT CCT GAA AGC CAA GAA CGC AGG GAT

450  
val ala gly gly gln gly arg arg arg pro ser ala leu arg gly  
GTC GCT GGG GGC CAA GGG CGC CGC CGG CCC TCT GCC CTC CGA GGC

460 470  
arg ala val ala val pro pro ser ile pro ala gln ala asp ser  
CGT GCA GTG GCT GTG CCA CCA AGC ATT CCT GCT CAA GCT GAC TCG

480  
thr pro cys his leu arg ala thr pro gly val thr gln asp ser  
ACA CCG TGT CAC CTA CGT GCC ACT CCT GGG GTC ACT CAG GAC AGC

490 500  
pro asp ala ala glu ser glu ala pro gly asp asp ala asp cys  
CCA GAC GCA GCT GAG TCG GAA GCT CCC GGG GAC GAC GCT GAC TGC

510  
pro gly gly arg ser gln pro gly thr ala leu arg leu gln asp  
CCT GGA GGC CGC AGC CAA CCC GGC ACT GCC CTC AGA CTT CAA GAC

520 530  
his pro gly leu met ala thr arg pro gln pro gly arg glu gln  
CAT CCT GGA CTG ATG GCC ACC CGC CCA CAG CCA GGC CGA GAG CAG

540  
thr pro ala ala leu ser arg arg ala tyr thr ser gln gly gly  
ACA CCA GCA GCC CTG TCA CGC CGG GCT TAT ACG TCC CAG GGA GGG

550 560  
arg gly gly pro his pro gly leu his arg trp glu ser glu ala  
AGG GGC GGC CCA CAC CCA GGC CTG CAC CGC TGG GAG TCT GAG GCC

564  
OP  
TGA GTGAGTGTTTGGCCGAGGCCTGCATGTCCGGCTGAAGGCTGAGTGTCGGCTGAGGC  
CTGAGCGAGTGTCAGCCAAGGGCTGAGTGTCAGCACACCTGCGTTTTCACTTCCCCAC  
AGGCTGGCGTTTCGGTCCACCCAGGGCCAGCTTTTCCTCACCAGGAGCCCGGCTTCCACT  
CCCCACATAGGAATAGTCCATCCCCAGATTGCGCCATTGTTCACCCCTTCGCCCTGCCTTCC  
TTTGCCTTCCACCCCCACCATTCAGGTGGAGACCCTGAGAAGGACCCTGGGAGCTTTGGG  
AATTTGGAGTGACCAAAGGTGTGCCCTGTACACAGGCGAGGACCCTGCACCTGGATGGGG  
GTCCCTGTGGGTCAAATTGGGGGGAGGTGCTGTGGGAGTAAAATACTGAATATATGAGTT  
TTTCAGTTTTTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIG. 68  
(CONTINUED)

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84/103

Motif -1  
Ep p123  
Sp Tez1  
Sc Est2  
Hs TCP1  
consensus

...LVVSLIRCFFYVTEQQKSYSKT...  
...FIIPILQSFFYITESSDLRNRT...  
...LIPKIIQTFFYCTEISSTVTIV...  
...YVVELLRSFFYVTETTFQKNRL...  
FFY TE

Motif 0  
Ep p123  
Sp Tez1  
Sc Est2  
Hs TCP1  
consensus

...KSLGFAPGKLRLIPKKT--TFRPIMTFNKKIV...  
...QKTTLPPAVIRLLPKKN--TFRLLITNLRKRFL...  
...TLSNFNHSMRIIPKKSNEFRIIAIPCRGAD...  
...ARPALLTSRLRFIPKPD--GLRPVNMMDYVVG...  
R PK R I

Motif A  
Ep p123  
Sp Tez1  
Sc Est2  
Hs TCP1  
consensus

...PKLFFATMDIEKCYDSVNREKLSTFLK...  
...RKKYFVRIDIKSCYDRIKQDLMFRIVK...  
...PELYFMKFVDVKSCYDSIPRMECMRILK...  
...PELYFVKVDVTGAYDTIPQDRLTEVIA...//...  
F D YD

Motif B  
Ep p123  
Sp Tez1  
Sc Est2  
Hs TCP1  
consensus

...NGKFYKQTKGIPQGLCVSSILSSFYYA...  
...GNSQYLQKVGIPQGSILSSFLCHFYME...  
...EDKCYIREDGLFQGSLSAPIVDLVYD...  
...RATSYVQCQGIPQGSILSTLLCSLCYG...  
G QG S

Motif C  
Ep p123  
Sp Tez1  
Sc Est2  
Hs TCP1  
consensus

...PNVNLLMRLTDDYLLITTQENN...  
...KKGSVLLRVDDFLFITVNKKD...  
...SQDTLILKLADDFLIISTDQQQ...  
...RRDGLLLRLVDDFLLVTPHLTH...  
DD L

Motif D  
Ep p123  
Sp Tez1  
Sc Est2  
Hs TCP1  
consensus

...NVSRENGFKFNMKKL...  
...LNLSLRGFEKHNFS...  
...KKLAMGGFQKYNAKA...  
...LRTLVRGVPEYGCVV...  
G

FIG. 69

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85/103

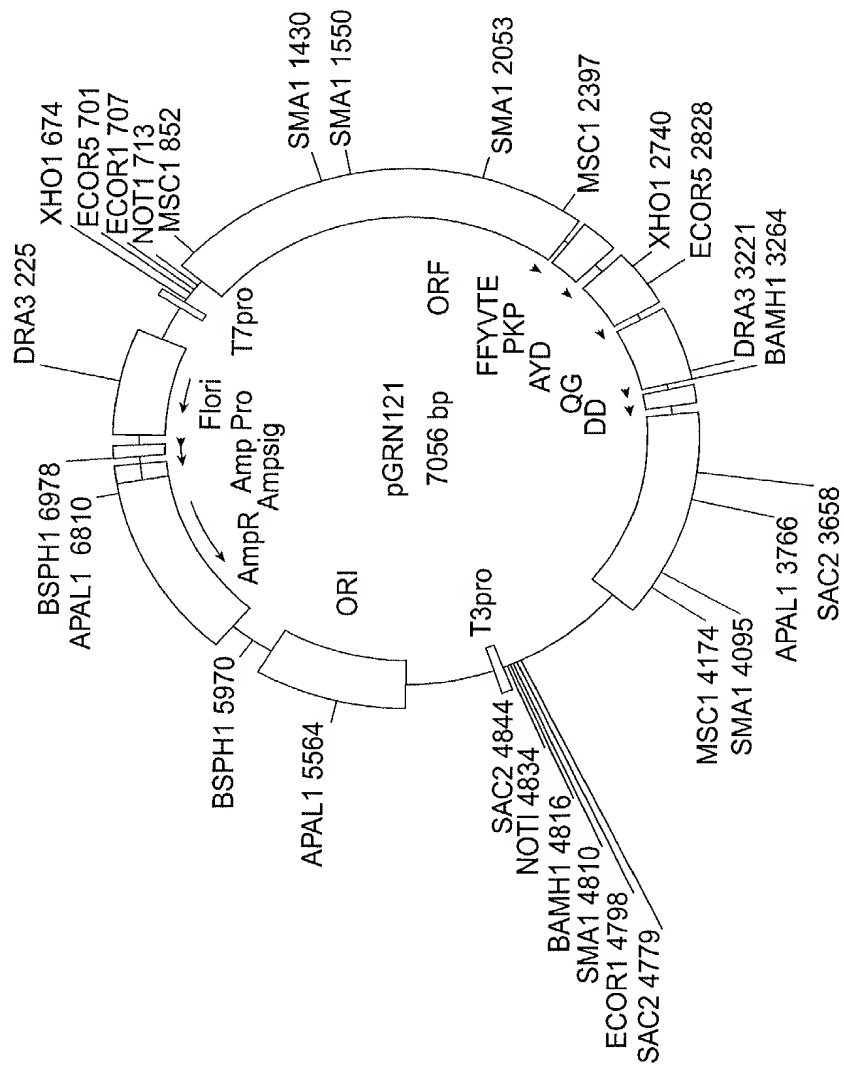


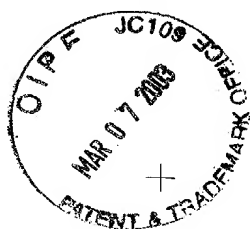
FIG. 70



86/103

1	GCAGCGCTGC	GTCCTGCTGC	GCACGTGGGA	AGCCCTGGCC	CCGGCCACCC
51	CCGCGATGCC	GCGCGCTCCC	CGCTGCCGAG	CCGTGCGCTC	CCTGCTGCGC
101	AGCCACTACC	GCGAGGTGCT	GCCGCTGGCC	ACGTTTCGTG	GGCGCCTGGG
151	GCCCCAGGGC	TGGCGGCTGG	TGCAGCGCGG	GGACCCGGCG	GCTTTCCGCG
201	CGNTGGTGGC	CCANTGCNTG	GTGTGCGTGC	CCTGGGANGN	ANGGCNGCCC
251	CCCGCCGCCC	CCTCCTTCCG	CCAGGTGTCC	TGCCTGAANG	ANCTGGTGGC
301	CCGAGTGCTG	CANANGCTGT	GCGANCGCGG	CGCGAANAAC	GTGCTGGCCT
351	TCGGCTTCGC	GCTGCTGGAC	GGGGCCCCGG	GGGGCCCCCC	CGAGGCCTTC
401	ACCACCAGCG	TGCGCAGCTA	CCTGCCCAAC	ACGGTGACCG	ACGCACTGCG
451	GGGGAGCGGG	GCGTGCGGGC	TGCTGCTGCG	CCGCGTGGGC	GACGACGTGC
501	TGGTTCACCT	GCTGGCACGC	TGCGCGNTNT	TTGTGCTGGT	GGNTCCCGAG
551	TGCGCCTACC	ANGTGTGCGG	GCCGCCGCTG	TACCAGCTCG	GCGCTGCNAC
601	TCAGGCCCGG	CCCCCGCCAC	ACGCTANTGG	ACCCGAANGC	GTCTGGGATC
651	CAACGGGCCT	GGAACCATAG	CGTCAGGGAG	GCCGGGGTCC	CCCTGGGCTG
701	CCAGCCCCGG	GTGCGAGGAG	GCGCGGGGGC	AGTGCCAGCC	GAAGTCTGCC
751	GTTGCCCAAG	AGGCCAGGCG	GTGGCGCTGC	CCCTGAGCCG	GAGCGGACGC
801	CCGTGGGGCA	GGGGTCCTGG	GCCCACCCGG	GCAGGACGCC	TGGACCGAGT
851	GACCGTGTTT	TCTGTGTGGT	GTCACCTGCC	AGACCCGCCG	AAGAAGCCAC
901	CTCTTTGGAG	GGTGCGCTCT	CTGGCACGCG	CCACTCCCAC	CCATCCGTGG
951	GCCGCCAGCA	CCACGCGGGC	CCCCCATCCA	CATCGCGGCC	ACCACGTCCT
1001	GGGACACGCC	TTGTCCCCCG	GTGTACGCCG	AGACCAAGCA	CTTCCTCTAC
1051	TCCTCAGGCG	ACAAGNACAC	TGCGNCCCTC	CTTCCTACTC	AATATATCTG
1101	AGGCCAGGCC	TGACTGGCGT	TCGGGAGGTT	CGTGGAGACA	NTCTTTCTGG
1151	TTCCAGGCCT	TGGATGCCAG	GATTCCCCGC	AGGTTGCCCC	GCCTGCCCCA
1201	GCGNTACTGG	CAAATGCGGC	CCCTGTTTCT	GGAGCTGCTT	GGGAACCACG
1251	CGCAGTGCCC	CTACGGGGTG	TTCCTCAAGA	CGCACTGCCC	GCTGCGAGCT
1301	GCGGTCACCC	CAGCAGCCGG	TGTCTGTGCC	CGGGAGAAGC	CCAGGGCTTC
1351	TGTGGCGGCC	CCCGAGGAGG	AGGAACACAG	ACCCCGTCTG	CCTGGTGCAG
1401	CTGCTCCGCC	AGCACAGCAG	CCCCTGGCAG	GTGTACGGCT	TCGTGCGGGC
1451	CTGCCTGCGC	CGGCTGGTGC	CCCCAGGCCT	CTGGGGCTCC	AGGCACAACG
1501	AACGCCGCTT	CCTCAGGAAC	ACCAAGAAGT	TCATCTCCCT	GGGGAAGCAT
1551	GCCAAGCTCT	CGCTGCAGGA	GCTGACGTGG	AAGATGAGCG	TGCGGGACTG
1601	CGCTTGGCTG	CGCAGGAGCC	CAGGGGTTGG	CTGTGTTCCG	GCCGCAGAGC
1651	ACCGTCTGCG	TGAGGAGATC	CTGGCCAAGT	TCCTGCACTG	GCTGATGAGT
1701	GTGTACGTCG	TCGAGCTGCT	CAGGTCTTTC	TTTTATGTCA	CGGAGACCAC
1751	GTTTTCAAAAG	AACAGGCTCT	TTTTCTACCG	GAAGAGTGTC	TGGAGCAAGT
1801	TGCAAAAGCAT	TGGAATCAGA	CAGCACTTGA	AGAGGGTGCA	GCTGCGGGAG
1851	CTGTGCGAAG	CAGAGGTCAG	GCAGCATCGG	GAAGCCAGGC	CCGCCCTGCT
1901	GACGTCCAGA	CTCCGCTTCA	TCCCCAAGCC	TGACGGGCTG	CGGCCGATTG
1951	TGAACATGGA	CTACGTCGTG	GGAGCCAGAA	CGTTCCGCAG	AGAAAAGAGG
2001	GCCGAGCGTC	TCACCTCGAG	GGTGAAGGCA	CTGTTACGCG	TGCTCAACTA
2051	CGAGCGGGCG	CGGCGCCCCG	GCCTCCTGGG	CGCCTCTGTG	CTGGGCCTGG
2101	ACGATATCCA	CAGGGCCTGG	CGCACCTTCG	TGCTGCGTGT	GCGGGCCCAG
2151	GACCCGCCGC	CTGAGCTGTA	CTTTGTCAAG	GTGGATGTGA	CGGGCGCGTA
2201	CGACACCATC	CCCCAGGACA	GGCTCACGGA	GGTCATCGCC	AGCATCATCA
2251	AACCCCAGAA	CACGTACTGC	GTGCGTCGGT	ATGCCGTGGT	CCAGAAGGCC
2301	GCCCATGGGC	ACGTCCGCAA	GGCCTTCAAG	AGCCACGTCT	CTACCTTGAC
2351	AGACCTCCAG	CCGTACATGC	GACAGTTCGT	GGCTCACCTG	CAGGANAACA
2401	GCCCCGCTGAG	GGATGCCGTC	GTCATCGAGC	AGAGCTCCTC	CCTGAATGAG
2451	GCCAGCAGTG	GCCTCTTCGA	CGTCTTCCTA	CGCTTCATGT	GCCACCACGC

FIG. 71



87/103

2501	CGTGCGCATC	AGGGGCAAGT	CCTACGTCCA	GTGCCAGGGG	ATCCCGCAGG
2551	GCTCCATCCT	CTCCACGCTG	CTCTGCAGCC	TGTGCTACGG	CGACATGGAG
2601	AACAAGCTGT	TTGCGGGGAT	TCGGCGGGAC	GGGCTGCTCC	TGCGTTTGGT
2651	GGATGATTTC	TTGTTGGTGA	CACCTCACCT	CACCCACGCG	AAAACCTTCC
2701	TCAGGACCCT	GGTCCGAGGT	GTCCCTGAGT	ATGGCTGCGT	GGTGAAC TTG
2751	CGGAAGACAG	TGGTGAAC TT	CCCTGTAGAA	GACGAGGCC	TGGGTGGCAC
2801	GGCTTTTGT	CAGATGCCGG	CCCACGGCCT	ATTCCCCTGG	TGCGGCC TGC
2851	TGCTGGATAC	CCGGACCCTG	GAGGTGCAGA	GCGACTACTC	CAGCTATGCC
2901	CGGACCTCCA	TCAGAGCCAG	TCTCACCTTC	AACCGCGGCT	TCAAGGCTGG
2951	GAGGAACATG	CGTCGCAAA	TCTTTGGGGT	CTTGCGGCTG	AAGTGTCACA
3001	GCCTGTTTCT	GGATTTGCAG	GTGAACAGCC	TCCAGACGGT	GTGCACCAAC
3051	ATCTACAAGA	TCCTCCTGCT	GCAGGCGTAC	AGGTTTCACG	CATGTGTGCT
3101	GCAGCTCCCA	TTTCATCAGC	AAGTTTGGAA	GAACCCACAC	TTTTTCCTGC
3151	GCGTCATCTC	TGACACGGCC	TCCCTCTGCT	ACTCCATCCT	GAAAGCCAAG
3201	AACGCAGGGA	TGTCGCTGGG	GGCCAAGGGC	GCCGCCGGCC	CTCTGCCCTC
3251	CGAGGCCGTG	CAGTGGCTGT	GCCACCAAGC	ATTCCTGCTC	AAGCTGACTC
3301	GACACCGTGT	CACCTACGTG	CCACTCCTGG	GGTCACTCAG	GACAGCCAG
3351	ACGCAGCTGA	GTCGGAAGCT	CCCGGGGACG	ACGCTGACTG	CCCTGGAGGC
3401	CGCAGCCAAC	CCGGCACTGC	CCTCAGACTT	CAAGACCATC	CTGGACTGAT
3451	GGCCACCCGC	CCACAGCCAG	GCCGAGAGCA	GACACCAGCA	GCCCTGTCAC
3501	GCCGGGCTCT	ACGTCCCAGG	GAGGGAGGGG	CGGCCACAC	CCAGGCCCGC
3551	ACCGCTGGGA	GTCTGAGGCC	TGAGTGAGTG	TTTGCCGAG	GCCTGCATGT
3601	CCGGCTGAAG	GCTGAGTGTC	CGGCTGAGGC	CTGAGCGAGT	GTCCAGCCAA
3651	GGGCTGAGTG	TCCAGCACAC	CTGCCGTCTT	CACTTCCCCA	CAGGCTGGCG
3701	CTCGGCTCCA	CCCCAGGGCC	AGCTTTTCCT	CACCAGGAGC	CCGGCTTCCA
3751	CTCCCCACAT	AGGAATAGTC	CATCCCCAGA	TTCGCCATTG	TTCACCCCTC
3801	GCCCTGCCCT	CCTTTGCCTT	CCACCCCCAC	CATCCAGGTG	GAGACCCTGA
3851	GAAGGACCCT	GGGAGCTCTG	GGAATTTGGA	GTGACCAAAG	GTGTGCCCTG
3901	TACACAGGCG	AGGACCCTGC	ACCTGGATGG	GGGTCCCTGT	GGGTCAAATT
3951	GGGGGGAGGT	GCTGTGGGAG	TAAAATACTG	AATATATGAG	TTTTTCAGTT
4001	TTGAAAAAAA	AAAAAAAAAA	AAAAAAAAAA		

FIG. 71  
(CONTINUED)

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88/103

GCAGCGCTGCGTCCTGCTGCGCACGTGGGAAGCCCTGGCCCCGGCCACCCCCGCGATGCC  
1 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 60  
CGTCGCGACGCAGGACGACGCGTGCACCCCTTCGGGACCGGGGCCGGTGGGGGCGCTACGG

a A A L R P A A H V G S P G P G H P R D A -  
b Q R C V L L R T W E A L A P A T P A M P -  
c S A A S C C A R G K P W P R P P P R C R -

GCGCGCTCCCCGCTGCCGAGCCGTGCGCTCCCTGCTGCGCAGCCACTACCGCGAGGTGCT  
61 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 120  
CGCGCGAGGGGCGACGGCTCGGCACGCGAGGGACGACGCGTGGTGATGGGCGCTCCACGA

a A R S P L P S R A L P A A Q P L P R G A -  
b R A P R C R A V R S L L R S H Y R E V L -  
c A L P A A E P C A P C C A A T T A R C C -

GCCGCTGGCCACGTTTCGTGCGGCGCCTGGGGCCCCAGGGCTGGCGGTGGTGCAGCGCGG  
121 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 180  
CGGCGACCGGTGCAAGCACGCGCGGACCCCGGGTCCCGACCGCGACACGTCGCGCC

a A A G H V R A A P G A P G L A A G A A R -  
b P L A T F V R R L G P Q G W R L V Q R G -  
c R W P R S C G A W G P R A G G W C S A G -

GGACCCGGCGGCTTTCGCGCGNTGGTGGCCCCANTGCNTGGTGTGCGTGCCTGGGANGN  
181 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 240  
CCTGGGCGCGCGAAAGGCGCGNACCACCGGTNACGNACCACACGACGGGACCCNTCN

a G P G G F P R ? G G P ? ? G V R A L G ? -  
b D P A A F R A ? V A ? C ? V C V P W ? ? -  
c T R R L S A R W W P ? A W C A C P G ? ? -

ANGGCNGCCCCCGCGCCCCCTCCTTCGCCAGGTGTCTGCCTGAANGANCCTGGTGGC  
241 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 300  
TNCCGNCGGGGGGCGGCGGGGGAGGAAGGCGGTCCACAGGACGGACTTNCCTNGACCACCG

a ? A A P R R P L L P P G V L P E ? ? G G -  
b ? ? P P A A P S F R Q V S C L ? ? L V A -  
c G ? P P P P P P S A R C P A \* ? ? W W P -

CCGAGTGCTGCANANGCTGTGCGANCGCGCGCGAANAACGTGCTGGCCTTCGGCTTCGC  
301 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 360  
GGCTCACGACGTNTNCGACACGCTNCGCGCGCGCTTNTTGCACGACCGGAAGCCGAAGCG

a P S A A ? A V R ? R R E ? R A G L R L R -  
b R V L ? ? L C ? R G A ? N V L A F G F A -  
c E C C ? ? C A ? A A R ? T C W P S A S R -

GCTGCTGGACGGGGCGCGGGGGCCCCCGAGGCCTTCACCACCAGCGTGCAGCTA  
361 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 420  
CGACGACCTGCCCCGGGCGCCCCCGGGGGGGCTCCGGAAGTGGTGGTGCACGCGTCGAT

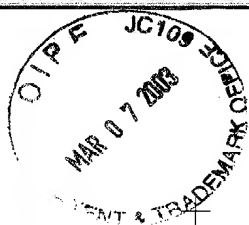
a A A G R G P R G P P R G L H H Q R A Q L -  
b L L D G A R G G P P E A F T T S V R S Y -  
c C W T G P A G A P P R P S P P A C A A T -

CCTGCCCAACACGGTGACCGACGCACTGCGGGGGAGCGGGCGTGGGGGCTGCTGCTGCG  
421 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 480  
GGACGGGTTGTGCCACTGGCTGCGTGACGCCCCCTCGCCCCGCACCCCGACGACGACG

a P A Q H G D R R T A G E R G V G A A A A -  
b L P N T V T D A L R G S G A W G L L L R -  
c C P T R \* P T H C G G A G R G G C C C A -

FIG. 72

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89/103

a P R G R R R A G S P A G T L R ? ? C A G -  
b R V G D D V L V H L L A R C A ? F V L V -  
c A W A T T C W F T C W H A A R ? L C W W -

541 GGNTCCCAGCTGCGCCTACCANGTGTGCGGGCCGCGCTGTACCAGCTCGGCGCTGCNAC  
-----+-----+-----+-----+-----+ 600  
CCNAGGGTCGACGCGGATGGTNCACACGCCCCGGCGGACATGGTTCGAGCCGCGACGNTG

a G S Q L R L P ? V R A A A V P A R R C ? -  
b ? P S C A Y ? V C G P P L Y Q L G A A T -  
c ? P A A P T ? C A G R R C T S S A L ? L -

601 TCAGGCCCCGCCCCGCCACACGCTANTGGACCCGAANGCGTCTGGGATCCAACGGGCCT  
-----+-----+-----+-----+-----+ 660  
AGTCCGGGCCGGGGCGGTGTGCGATNACCTGGGCTTNCGCAGACCCTAGGTTGCCCGGA

a S G P A P A T R ? W T R ? R L G S N G P -  
b Q A R P P P H A ? G P E ? V W D P T G L -  
c R P G P R H T L ? D P ? A S G I Q R A W -

661 GGAACCATAGCGTCAGGGAGGCCGGGGTCCCCCTGGGCTGCCAGCCCCGGGTGCGAGGAG  
-----+-----+-----+-----+-----+ 720  
CCTTGGTATCGCAGTCCCTCCGGCCCCAGGGGGACCCGACGGTTCGGGGCCACGCTCCTC

a G T I A S G R P G S P W A A S P G C E E -  
b E P \* R Q G G R G P P G L P A P G A R R -  
c N H S V R E A G V P L G C Q P R V R G G -

721 GCGCGGGGGCAGTGCCAGCCGAAGTCTGCCGTTGCCCAAGAGGCCAGGCGTGCGCTGC  
-----+-----+-----+-----+-----+ 780  
CGCGCCCCCGTACGGTTCGGCTTCAGACGGCAACGGGTTCTCCGGTCCGCACCGCGACG

a A R G Q C Q P K S A V A Q E A Q A W R C -  
b R G G S A S R S L P L P K R P R R G A A -  
c A G A V P A E V C R C P R G P G V A L P -

781 CCCTGAGCCGGAGCGGACGCCCCGTTGGGCAGGGGTCTGGGCCCCACCCGGGCAGGACGCC  
-----+-----+-----+-----+-----+ 840  
GGGACTCGGCCTCGCCTGCGGGCAACCGTCCCCAGGACCCGGGTGGGCCCCGTCTCGCG

a P \* A G A D A R W A G V L G P P G Q D A -  
b P E P E R T P V G Q G S W A H P G R T P -  
c L S R S G R P L G R G P G P T R A G R L -

841 TGGACCGAGTGACCGTGGTTTCTGTGTGGTGTACCTGCCAGACCCGCCGAAGAAGCCAC  
-----+-----+-----+-----+-----+ 900  
ACCTGGCTCACTGGCACCAGACACACCACAGTGGACGGTCTGGGCGGCTTCTTCGGTG

a W T E \* P W F L C G V T C Q T R R R S H -  
b G P S D R G F C V V S P A R P A E E A T -  
c D R V T V V S V W C H L P D P P K K P P -

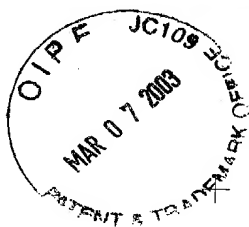
901 CTCTTTGGAGGGTGCGCTCTCTGGCACGCGCCACTCCCACCCATCCGTGGGCCGCCAGCA  
-----+-----+-----+-----+-----+ 960  
GAGAAACCTCCCACGCGAGAGACCGTGC GCGGTGAGGGTGGGTAGGCACCCGGCGGTCTG

a L F G G C A L W H A P L P P I R G P P A -  
b S L E G A L S G T R H S H P S V G R Q H -  
c L W R V R S L A R A T P T H P W A A S T -

961 CCACGCGGGCCCCCATCCACATCGCGGCCACACGTCCTGGGACACGCCTTGTCCTCCCCG  
-----+-----+-----+-----+-----+ 1020  
GGTGCGCCCCGGGGGTAGGTGTAGCGCCGTTGGTGCAGGACCCTGTGCGGAACAGGGGGC

FIG. 72  
(CONTINUED)

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90/103

a P R G P P I H I A A T T S W D T P C P P -  
b H A G P P S T S R P P R P G T R L V P R -  
c T R A P H P H R G H H V L G H A L S P G -

1021 GTGTACGCCGAGACCAAGCACTTCCTCTACTCCTCAGGCGACAAGNACACTGCGNCCCTC  
-----+-----+-----+-----+-----+-----+ 1080  
CACATGCGGCTCTGGTTTCGTGAAGGAGATGAGGAGTCCGCTGTTTCNTGTGACGCNCGGAG

a V Y A E T K H F L Y S S G D K ? T A ? L -  
b C T P R P S T S S T P Q A T ? T L R P S -  
c V R R D Q A L P L L L R R Q ? H C ? P P -

1081 CTTCCTACTCAATATATCTGAGGCCAGCCTGACTGGCGTTCGGGAGGTTCTGTGGAGACA  
-----+-----+-----+-----+-----+-----+ 1140  
GAAGGATGAGTTATATAGACTCCGGGTGCGACTGACCGCAAGCCCTCCAAGCACCTCTGT

a L P T Q Y I \* G P A \* L A F G R F V E T -  
b F L L N I S E A Q P D W R S G G S W R ? -  
c S Y S I Y L R P S L T G V R E V R G D ? -

1141 NTCTTTCTGGTTCCAGGCCTTGGATGCCAGGATTCCTCCGCGAGGTTGCCCGCCTGCCCA  
-----+-----+-----+-----+-----+-----+ 1200  
NAGAAAGACCAAGGTCCGGAACCTACGGTCTTAAGGGGCGTCCAACGGGGCGGACGGGT

a ? F L V P G L G C Q D S P Q V A P P A P -  
b S F W F Q A L D A R I P R R L P R L P Q -  
c L S G S R P W M P G F P A G C P A C P S -

1201 GCGNTACTGGCAAATGCGGCCCTGTTTCTGGAGCTGCTTGGGAACCACGCGCAGTGCCC  
-----+-----+-----+-----+-----+-----+ 1260  
CGCNATGACCGTTTACGCCGGGACAAAGACCTCGACGAACCCCTGGTGCGCGTCACGGG

a A ? L A N A A P V S G A A W E P R A V P -  
b R Y W Q M R P L F L E L L G N H A Q C P -  
c ? T G K C G P C F W S C L G T T R S A P -

1261 CTACGGGGTGTTCCTCAAGACGCACTGCCCGCTGCGAGCTGCGGTACCCCCAGCAGCCGG  
-----+-----+-----+-----+-----+-----+ 1320  
GATGCCCCACAAGGAGTTCTGCGTGACGGGCGACGCTCGACGCCAGTGGGGTCTGTCGCC

a L R G V P Q D A L P A A S C G H P S S R -  
b Y G V F L K T H C P L R A A V T P A A G -  
c T G C S S R R T A R C E L R S P Q Q P V -

1321 TGTCTGTGCCCCGGGAGAAGCCCCAGGGCTCTGTGGCGGCCCCGAGGAGGAACACAG  
-----+-----+-----+-----+-----+-----+ 1380  
ACAGACACGGGCCCTCTTCGGGGTCCCGAGACCCGCCGGGGCTCCTCCTCCTTGTGTC

a C L C P G E A P G L C G G P R G G G T Q -  
b V C A R E K P Q G S V A A P E E E E H R -  
c S V P G R S P R A L W R P P R R R N T D -

1381 ACCCCCGTCGCCTGGTGCAGCTGCTCCGCCAGCACAGCAGCCCTGGCAGGTGTACGGCT  
-----+-----+-----+-----+-----+-----+ 1440  
TGGGGGCAGCGGACCAGTCGACGAGGCGGTGCTGTCGTCGGGGACCGTCCACATGCCGA

a T P V A W C S C S A S T A A P G R C T A -  
b P P S P G A A A P P A Q Q P L A G V R L -  
c P R R L V Q L L R Q H S S P W Q V Y G F -

1441 TCGTGCGGGCCTGCCTGCGCCGGCTGGTGCCCCAGGCCTCTGGGGCTCCAGGCACAACG  
-----+-----+-----+-----+-----+-----+ 1500  
AGCACGCCCGGACGGACGCGGCCGACCACGGGGGTCCGGAGACCCCGAGGTCCGTGTTGC

FIG. 72  
(CONTINUED)

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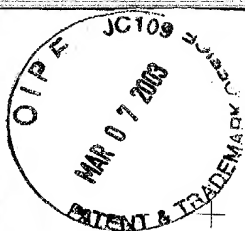


91/103

a S C G P A C A G W C P Q A S G A P G T T -  
b R A G L P A P A G A P R P L G L Q A Q R -  
c V R A C L R R L V P P G L W G S R H N E -  
  
AACGCCGCTTCCTCAGGAACACCAAGAAGTTTCATCTCCCTGGGGAAGCATGCCAAGCTCT  
1501 -----+-----+-----+-----+-----+ 1560  
TTGCGGCGAAGGAGTCCTTGTTGTTCTTCAAGTAGAGGGACCCCTTCGTACGGTTCGAGA  
  
a N A A S S G T P R S S S P W G S M P S S -  
b T P L P Q E H Q E V H L P G E A C Q A L -  
c R R F L R N T K K F I S L G K H A K L S -  
  
CGCTGCAGGAGCTGACGTGGAAGATGAGCGTGCGGGACTGCGCTTGGCTGCGCAGGAGCC  
1561 -----+-----+-----+-----+-----+ 1620  
GCGAGCTCCTCGACTGCACCTTCTACTCGCAGCCCTGACGCGAACCAGCGCTCCTCGG  
  
a R C R S \* R G R \* A C G T A L G C A G A -  
b A A G A D V E D E R A G L R L A A Q E P -  
c L Q E L T W K M S V R D C A W L R R S P -  
  
CAGGGGTTGGCTGTGTTCCGGCCGAGAGCACCCTCTGCGTGAGGAGATCCTGGCCAAGT  
1621 -----+-----+-----+-----+-----+ 1680  
GTCCCCAACCGACACAAGGCCGGCGTCTCGTGACAGCGCACTCCTCTAGGACCGGTTCA  
  
a Q G L A V F R P Q S T V C V R R S W P S -  
b R G W L C S G R R A P S A \* G D P G Q V -  
c G V G C V P A A E H R L R E E I L A K F -  
  
TCCTGCACTGGCTGATGAGTGTGTACGTGCTGAGCTGCTCAGGTCTTTCTTTTATGTCA  
1681 -----+-----+-----+-----+-----+ 1740  
AGGACGTGACCGACTACTCACATGCAGCAGCTCGACGAGTCCAGAAAGAAAATACAGT  
  
a S C T G \* \* V C T S S S C S G L S F M S -  
b P A L A D E C V R R R A A Q V F L L C H -  
c L H W L M S V Y V V E L L R S F F Y V T -  
  
CGGAGACCACGTTTCAAAAGAACAGGCTCTTTTCTACCGGAAGAGTGTCTGGAGCAAGT  
1741 -----+-----+-----+-----+-----+ 1800  
GCCTCTGGTGCAAAGTTTCTTGTCGAGAGAAAAGATGGCCTTCTCACAGACCTCGTTCA  
  
a R R P R F K R T G S F S T G R V S G A S -  
b G D H V S K E Q A L F L P E E C L E Q V -  
c E T T F Q K N R L F F Y R K S V W S K L -  
  
TGCAAAGCATTGGAATCAGACAGCACTTGAAGAGGGTGCAGCTGCGGGAGCTGTCCGAAG  
1801 -----+-----+-----+-----+-----+ 1860  
ACGTTTCGTAACTTAGTCTGTGTAACCTTCTCCACGTGACGCCCTCGACAGCCTTC  
  
a C K A L E S D S T \* R G C S C G S C R K -  
b A K H W N Q T A L E E G A A A G A V G S -  
c Q S I G I R Q H L K R V Q L R E L S E A -  
  
CAGAGGTCAGGCAGCATCGGGAAGCCAGGCCCGCCCTGCTGACGTCCAGACTCCGCTTCA  
1861 -----+-----+-----+-----+-----+ 1920  
GTCTCCAGTCCGTCGTAGCCCTTCGGTCCGGGCGGACGACTGCAGGTCTGAGGCGAAGT  
  
a Q R S G S I G K P G P P C \* R P D S A S -  
b R G Q A A S G S Q A R P A D V Q T P L H -  
c E V R Q H R E A R P A L L T S R L R F I -  
  
TCCCCAAGCCTGACGGGCTGCGGCCGATTGTGAACATGGACTACGTGCTGGGAGCCAGAA  
1921 -----+-----+-----+-----+-----+ 1980  
AGGGGTTTCGACTGCCCGACGCCGCTAACACTTGTACCTGATGCAGCACCCCTCGGTCTT

FIG. 72  
(CONTINUED)

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92/103

a S P S L T G C G R L \* T W T T S W E P E -  
b P Q A \* R A A A D C E H G L R R G S Q N -  
c P K P D G L R P I V N M D Y V V G A R T -  
  
CGTTCCGCAGAGAAAAGAGGGCCGAGCGTCTCACCTCGAGGGTGAAGGCACTGTTTCAGCG  
1981 -----+-----+-----+-----+-----+ 2040  
GCAAGGCGTCTCTTTTCTCCCGGCTCGCAGAGTGGAGCTCCCACTTCCGTGACAAGTCGC  
  
a R S A E K R G P S V S P R G \* R H C S A -  
b V P Q R K E G R A S H L E G E G T V Q R -  
c F R R E K R A E R L T S R V K A L F S V -  
  
TGCTCAACTACGAGCGGGCGCGGCGCCCGGCTCCTGGGCGCCTCTGTGCTGGGCTGG  
2041 -----+-----+-----+-----+-----+ 2100  
ACGAGTTGATGCTCGCCCGCGCCGCGGGGCGGAGACCCGCGGAGACACGACCCGCGACC  
  
a C S T T S G R G A P A S W A P L C W A W -  
b A Q L R A G A A P R P P G R L C A G P G -  
c L N Y E R A R R P G L L G A S V L G L D -  
  
ACGATATCCACAGGGCCTGGCGCACCTTCGTGCTGCGTGTGCGGGCCAGGACCCGCGCG  
2101 -----+-----+-----+-----+-----+ 2160  
TGCTATAGGTGTCCCGGACCGCGTGAAGCAGCAGCACACGCCCCGGGTCTTGGGCGCGC  
  
a T I S T G P G A P S C C V C G P R T R R -  
b R Y P Q G L A H L R A A C A G P G P A A -  
c D I H R A W R T F V L R V R A Q D P P P -  
  
CTGAGCTGTACTTTGTCAAGGTGGATGTGACGGGCGCGTACGACACCATCCCCCAGGACA  
2161 -----+-----+-----+-----+-----+ 2220  
GACTCGACATGAAACAGTTCACCTACACTGCCCGCGCATGCTGTGGTAGGGGTCTCTGT  
  
a L S C T L S R W M \* R A R T T P S P R T -  
b \* A V L C Q G G C D G R V R H H P P G Q -  
c E L Y F V K V D V T G A Y D T I P Q D R -  
  
GGCTCACGGAGGTCATCGCCAGCATCATCAAACCCAGAACACGTACTGCGTGCCTCGGT  
2221 -----+-----+-----+-----+-----+ 2280  
CCGAGTGCCCTCCAGTAGCGGTCTAGTAGTTTGGGGTCTTGTGCATGACGCACGCAGCCA  
  
a G S R R S S P A S S N P R T R T A C V G -  
b A H G G H R Q H H Q T P E H V L R A S V -  
c L T E V I A S I I K P Q N T Y C V R R Y -  
  
ATGCCGTGGTCCAGAAGGCCGCCCATGGGCACGTCCGCAAGGCCTTCAAGAGCCACGTCT  
2281 -----+-----+-----+-----+-----+ 2340  
TACGGCACCAGGTCTTCCGGCGGGTACCCGTGCAGGCGTTCCGGAAGTTCTCGGTGCAGA  
  
a M P W S R R P P M G T S A R P S R A T S -  
b C R G P E G R P W A R P Q G L Q E P R L -  
c A V V Q K A A H G H V R K A F K S H V S -  
  
CTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTCGTGGCTCACCTGCAGGANAACA  
2341 -----+-----+-----+-----+-----+ 2400  
GATGGAACGTGTCTGGAGGTCCGCATGTACGTGTCAAGCACCGAGTGGACGTCTNTTGT  
  
a L P \* Q T S S R T C D S S W L T C R ? T -  
b Y L D R P P A V H A T V R G S P A G ? Q -  
c T L T D L Q P Y M R Q F V A H L Q ? N S -  
  
GCCCCGTGAGGGATGCCGTGTCATCGAGCAGAGCTCCTCCCTGAATGAGGCCAGCAGTG  
2401 -----+-----+-----+-----+-----+ 2460  
CGGGCGACTCCCTACGGCAGCAGTAGCTCGTCTCGAGGAGGGACTTACTCCGGTCGTAC

FIG. 72  
(CONTINUED)

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93/103

a A R \* G M P S S S S R A P P \* M R P A V -  
b P A E G C R R H R A E L L P E \* G Q Q W -  
c P L R D A V V I E Q S S S L N E A S S G -  
GCCTCTTCGACGTCTTCCTACGCTTCATGTGCCACCACGCCGTGCGCATCAGGGGCAAGT  
2461 -----+-----+-----+-----+-----+-----+ 2520  
CGGAGAAGCTGCAGAAGGATGCGAAGTACACGGTGGTGGCGCACGCGTAGTCCCCGTTCA  
a A S S T S S Y A S C A T T P C A S G A S -  
b P L R R L P T L H V P P R R A H Q G Q V -  
c L F D V F L R F M C H H A V R I R G K S -  
CCTACGTCCAGTGCCAGGGGATCCCGCAGGGCTCCATCCTCTCCACGTGCTCTGCAGCC  
2521 -----+-----+-----+-----+-----+-----+ 2580  
GGATGCAGGTACCGGTCCCCTAGGGCGTCCCGAGGTAGGAGAGGTGCGACGAGACGTCCG  
a P T S S A R G S R R A P S S P R C S A A -  
b L R P V P G D P A G L H P L H A A L Q P -  
c Y V Q C Q G I P Q G S I L S T L L C S L -  
TGTGCTACGGCGACATGGAGAACAAGCTGTTTTGCGGGGATTTCGGCGGGACGGGCTGCTCC  
2581 -----+-----+-----+-----+-----+-----+ 2640  
ACACGATGCCGCTGTACCTCTTGTTCGACAAACGCCCCCTAAGCCGCCCTGCCCGACGAGG  
a C A T A T W R T S C L R G F G G T G C S -  
b V L R R H G E Q A V C G D S A G R A A P -  
c C Y G D M E N K L F A G I R R D G L L L -  
TGCGTTTGGTGGATGATTTCTTGTGGTGACACCTCACCTCACCCACGCGAAAACCTTCC  
2641 -----+-----+-----+-----+-----+-----+ 2700  
ACGCAAACCACCTACTAAAGAACAACCACTGTGGAGTGGAGTGGGTGCGCTTTTGAAGG  
a C V W W M I S C W \* H L T S P T R K P S -  
b A F G G \* F L V G D T S P H P R E N L P -  
c R L V D D F L L V T P H L T H A K T F L -  
TCAGGACCTGGTCCGAGGTGTCCCTGAGTATGGCTGCGTGGTGAACCTGCGGAAGACAG  
2701 -----+-----+-----+-----+-----+-----+ 2760  
AGTCCTGGGACCAGGCTCCACAGGGACTCATACCGACGCACCACCTGAACGCCCTTCTGTCT  
a S G P W S E V S L S M A A W \* T C G R Q -  
b Q D P G P R C P \* V W L R G E L A E D S -  
c R T L V R G V P E Y G C V V N L R K T V -  
TGGTGAACCTTCCCTGTAGAAGACGAGGGCCCTGGGTGGCACGGCTTTTGTTCAGATGCCGG  
2761 -----+-----+-----+-----+-----+-----+ 2820  
ACCACTTGAAGGGACATCTTCTGCTCCGGGACCCACCGTGCCGAAAACAAGTCTACGGCC  
a W \* T S L \* K T R P W V A R L L F R C R -  
b G E L P C R R R G P G W H G F C S D A G -  
c V N F P V E D E A L G G T A F V Q M P A -  
CCACAGGCCTATTCCCTGGTGGCGCCTGCTGCTGGATACCCGGACCCCTGGAGGTGCAGA  
2821 -----+-----+-----+-----+-----+-----+ 2880  
GGGTGCCGATAAGGGGACCACGCCGACGACCTATGGGCCTGGGACCTCCACGTCT  
a P T A Y S P G A A C C W I P G P W R C R -  
b P R P I P L V R P A A G Y P D P G G A E -  
c H G L F P W C G L L L D T R T L E V Q S -  
GCGACTACTCCAGCTATGCCCGGACCTCCATCAGAGCCAGTCTCACCTTCAACCGCGGCT  
2881 -----+-----+-----+-----+-----+-----+ 2940  
CGCTGATGAGGTGCATACGGGCCTGGAGGTAGTCTCGGTCAGAGTGGAAGTTGGCGCCGA

FIG. 72  
(CONTINUED)

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94/103

a A T T P A M P G P P S E P V S P S T A A -  
b R L L Q L C P D L H Q S Q S H L Q P R L -  
c D Y S S Y A R T S I R A S L T F N R G F -  
TCAAGGCTGGGAGGAACATGCGTCGCAAACTCTTTGGGGTCTTGCGGCTGAAGTGTCACA  
2941 -----+-----+-----+-----+-----+ 3000  
AGTTCCGACCCTCCTTGTACGCAGCGTTTGAGAAACCCAGAACGCCGACTTCACAGTGT  
a S R L G G T C V A N S L G S C G \* S V T -  
b Q G W E E H A S Q T L W G L A A E V S Q -  
c K A G R N M R R K L F G V L R L K C H S -  
GCCTGTTTCTGGATTTCAGGTGAACAGCCTCCAGACGGTGTGCACCAACATCTACAAGA  
3001 -----+-----+-----+-----+-----+ 3060  
CGGACAAAGACCTAAACGTCCACTTGTGCGAGGTCTGCCACACGTGGTTGTAGATGTTCT  
a A C F W I C R \* T A S R R C A P T S T R -  
b P V S G F A G E Q P P D G V H Q H L Q D -  
c L F L D L Q V N S L Q T V C T N I Y K I -  
TCCTCCTGCTGCAGGCGTACAGGTTTCACGCATGTGTGCTGCAGCTCCCATTTTCATCAGC  
3061 -----+-----+-----+-----+-----+ 3120  
AGGAGGACGACGTCCGCATGTCCAAAGTGCGTACACACGACGTGAGGGTAAAGTAGTCG  
a S S C C R R T G F T H V C C S S H F I S -  
b P P A A G V Q V S R M C A A A P I S S A -  
c L L L Q A Y R F H A C V L Q L P F H Q Q -  
AAGTTTGAAGAACCCACATTTTTCCTGCGCGTCATCTCTGACACGGCCTCCCTCTGCT  
3121 -----+-----+-----+-----+-----+ 3180  
TTCAAACCTTCTTGGGGTGTAAAAAGGACGCGCAGTAGAGACTGTGCCGGAGGGAGACGA  
a K F G R T P H F S C A S S L T R P P S A -  
b S L E E P H I F P A R H L \* H G L P L L -  
c V W K N P T F F L R V I S D T A S L C Y -  
ACTCCATCCTGAAAGCCAAGAACGCAGGGATGTGCTGGGGGCCAAGGGCGCCGCCGCC  
3181 -----+-----+-----+-----+-----+ 3240  
TGAGGTAGGACTTTTCGGTTCTTGCGTCCCTACAGCGACCCCCGGTTCGCCGGCGGCCGG  
a T P S \* K P R T Q G C R W G P R A P P A -  
b L H P E S Q E R R D V A G G Q G R R R P -  
c S I L K A K N A G M S L G A K G A A G P -  
CTCTGCCCTCCGAGGCCGTGCGAGTGGCTGTGCCACCAAGCATTCTGCTCAAGCTGACTC  
3241 -----+-----+-----+-----+-----+ 3300  
GAGACGGGAGGCTCCGGCACGTCACCGACACGGTGGTTTCGTAAGGACGAGTTCGACTGAG  
a L C P P R P C S G C A T K H S C S S \* L -  
b S A L R G R A V A V P P S I P A Q A D S -  
c L P S E A V Q W L C H Q A F L L K L T R -  
GACACCGTGTACCTACGTGCCACTCCTGGGGTCACTCAGGACAGCCCAGACGCAGCTGA  
3301 -----+-----+-----+-----+-----+ 3360  
CTGTGGCACAGTGGATGCACGGTGAGGACCCAGTGAGTCCTGTCGGGTCTGCGTCGACT  
a D T V S P T C H S W G H S G Q P R R S \* -  
b T P C H L R A T P G V T Q D S P D A A E -  
c H R V T Y V P L L G S L R T A Q T Q L S -  
GTCGGAAGCTCCCGGGGACGACGCTGACTGCCCTGGAGGCCGAGCCAACCCGGCACTGC  
3361 -----+-----+-----+-----+-----+ 3420  
CAGCCTTCGAGGGGCCCTGCTGCGACTGACGGGACCTCCGGCGTCGGTTGGGCCGTGACG

FIG. 72  
(CONTINUED)

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95/103

a V G S S R G R R \* L P W R P Q P T R H C -  
b S E A P G D D A D C P G G R S Q P G T A -  
c R K L P G T T L T A L E A A A N P A L P -  
  
CCTCAGACTTCAAGACCATCCTGGACTGATGGCCACCCGCCACAGCCAGGCCGAGAGCA  
3421 -----+-----+-----+-----+-----+ 3480  
GGAGTCTGAAGTTCTGGTAGGACCTGACTACCGGTGGGCGGGTGTCTGGTCCGGCTCTCGT  
  
a P Q T S R P S W T D G H P P T A R P R A -  
b L R L Q D H P G L M A T R P Q P G R E Q -  
c S D F K T I L D \* W P P A H S Q A E S R -  
  
GACACCAGCAGCCCTGTCTACGCCGGGCTCTACGTCCCAGGGAGGGAGGGGCGGCCACAC  
3481 -----+-----+-----+-----+-----+ 3540  
CTGTGGTCTGTCGGACAGTGCGCCCGAGATGCAGGTCCCTCCCTCCCCGCCGGGTGTG  
  
a D T S S P V T P G S T S Q G G R G G P H -  
b T P A A L S R R A L R P R E G G A A H T -  
c H Q Q P C H A G L Y V P G R E G R P T P -  
  
CCAGGCCCCGACCGCTGGGAGTCTGAGGCCTGAGTGAGTGTGTTGGCCGAGGCCTGCATGT  
3541 -----+-----+-----+-----+-----+ 3600  
GGTCCGGGCGTGGCGACCTCAGACTCCGGACTCACTCACAAACCGGCTCCGGACGTACA  
  
a P G P H R W E S E A \* V S V W P R P A C -  
b Q A R T A G S L R P E \* V F G R G L H V -  
c R P A P L G V \* G L S E C L A E A C M S -  
  
CCGGCTGAAGGCTGAGTGTCCGGCTGAGGCCTGAGCGAGTGTCCAGCCAAGGGCTGAGTG  
3601 -----+-----+-----+-----+-----+ 3660  
GGCCGACTTCCGACTCACAGGCCGACTCCGGACTCGCTCACAGGTCTGGTTCCTCCGACTCAC  
  
a P A E G \* V S G \* G L S E C P A K G \* V -  
b R L K A E C P A E A \* A S V Q P R A E C -  
c G \* R L S V R L R P E R V S S Q G L S V -  
  
TCCAGCACACCTGCCGTCTTCACTTCCCCACAGGCTGGCGCTCGGCTCCACCCCAGGGCC  
3661 -----+-----+-----+-----+-----+ 3720  
AGGTCTGTGGACGGCAGAAAGTGAAGGGGTGTCCGACCGCGAGCCGAGGTGGGGTCCCGG  
  
a S S T P A V F T S P Q A G A R L H P R A -  
b P A H L P S S L P H R L A L G S T P G P -  
c Q H T C R L H F P T G W R S A P P Q G Q -  
  
AGCTTTTCTCTACCCAGGAGCCCGGCTTCCACTCCCCACATAGGAATAGTCCATCCCCAGA  
3721 -----+-----+-----+-----+-----+ 3780  
TCGAAAAGGAGTGGTCTCTCGGGCCGAAGGTGAGGGGTGTATCCTTATCAGGTAGGGGTCT  
  
a S F S S P G A R L P L P T \* E \* S I P R -  
b A F P H Q E P G F H S P H R N S P S P D -  
c L F L T R S P A S T P H I G I V H P Q I -  
  
TTCGCCATTGTTTACCCCTCGCCCTGCCCTTCTTTGCCTTCCACCCCCACCATCCAGGTG  
3781 -----+-----+-----+-----+-----+ 3840  
AAGCGGTAACAAGTGGGAGCGGGACGGGAGGAAACGGAAGGTGGGGGTGGTAGGTCCAC  
  
a F A I V H P S P C P P L P S T P T I Q V -  
b S P L F T P R P A L L C L P P P P S R W -  
c R H C S P L A L P S F A F H P H H P G G -  
  
GAGACCCTGAGAAGGACCCTGGGAGCTCTGGGAATTTGGAGTGACCAAAGGTGTGCCCTG  
3841 -----+-----+-----+-----+-----+ 3900  
CTCTGGGACTCTTCTGGGACCCTCGAGACCCTTAAACCTCACTGGTTTCCACACGGGAC

FIG. 72  
(CONTINUED)

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96/103

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a      E T L R R T L G A L G I W S D Q R C A L -
b      R P * E G P W E L W E F G V T K G V P C -
c      D P E K D P G S S G N L E * P K V C P V -

TACACAGGCGAGGACCCCTGCACCTGGATGGGGGTCCCTGTGGGTCAAATTGGGGGGAGGT
3901 -----+-----+-----+-----+-----+ 3960
ATGTGTCCGCTCCTGGGACGTGGACCTACCCCCAGGGACACCCAGTTTAACCCCCCTCCA

a      Y T G E D P A P G W G S L W V K L G G G -
b      T Q A R T L H L D G G P C G S N W G E V -
c      H R R G P C T W M G V P V G Q I G G R C -

GCTGTGGGAGTAAAAATACTGAATATATGAGTTTTTCAGTTTTTGAAAAAAAAAAAAAAAA
3961 -----+-----+-----+-----+-----+ 4020
CGACACCCCTCATTTTATGACTTATATACTCAAAAAGTCAAAACTTTTTTTTTTTTTTTT

a      A V G V K Y * I Y E F F S F E K K K K K -
b      L W E * N T E Y M S F S V L K K K K K -
c      C G S K I L N I * V F Q F * K K K K K -

AAAAA
4021 ----- 4029
TTTTTTTTT

a      K K K -
b      K K -
c      K K -
```

FIG. 72  
(CONTINUED)

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97/103

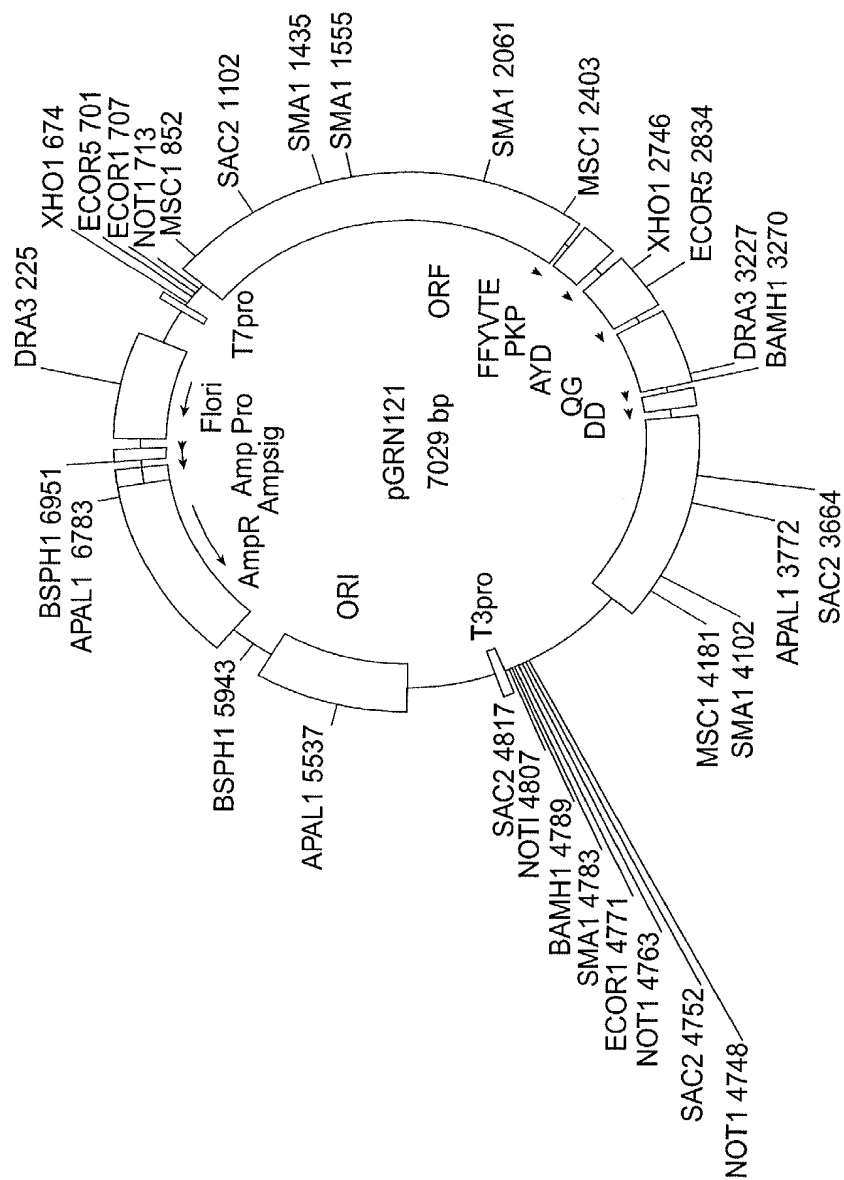


FIG. 73

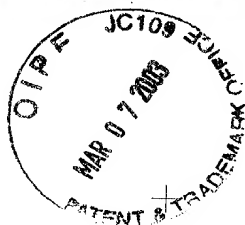


98/103

GCAGCGCTGCGTCCTGCTGCGCACGTGGGAAGCCCTGGCCCCGGCCACCCCCGCG ATG<sup>1</sup>  
met  
10  
pro arg ala pro arg cys arg ala val arg ser leu leu arg ser  
CCG CGC GCT CCC CGC TGC CGA GCC GTG CGC TCC CTG CTG CGC AGC  
20 30  
his tyr arg glu val leu pro leu ala thr phe val arg arg leu  
CAC TAC CGC GAG GTG CTG CCG CTG GCC ACG TTC GTG CGG CGC CTG  
40  
gly pro gln gly trp arg leu val gln arg gly asp pro ala ala  
GGG CCC CAG GGC TGG CGG CTG GTG CAG CGC GGG GAC CCG GCG GCT  
50 60  
phe arg ala leu val ala gln cys leu val cys val pro trp asp  
TTC CGC GCG CTG GTG GCC CAG TGC CTG GTG TGC GTG CCC TGG GAC  
70  
ala arg pro pro pro ala ala pro ser phe arg gln val ser cys  
GCA CGG CCG CCC CCC GCC GCC CCC TCC TTC CGC CAG GTG TCC TGC  
80 90  
leu lys glu leu val ala arg val leu gln arg leu cys glu arg  
CTG AAG GAG CTG GTG GCC CGA GTG CTG CAG AGG CTG TGC GAG CGC  
100  
gly ala lys asn val leu ala phe gly phe ala leu leu asp gly  
GGC GCG AAG AAC GTG CTG GCC TTC GGC TTC GCG CTG CTG GAC GGG  
110 120  
ala arg gly gly pro pro glu ala phe thr thr ser val arg ser  
GCC CGC GGG GGC CCC CCC GAG GCC TTC ACC ACC AGC GTG CGC AGC  
130  
tyr leu pro asn thr val thr asp ala leu arg gly ser gly ala  
TAC CTG CCC AAC ACG GTG ACC GAC GCA CTG CGG GGG AGC GGG GCG  
140 150  
trp gly leu leu leu arg arg val gly asp asp val leu val his  
TGG GGG CTG CTG CTG CGC CGC GTG GGC GAC GAC GTG CTG GTT CAC  
160  
leu leu ala arg cys ala leu phe val leu val ala pro ser cys  
CTG CTG GCA CGC TGC GCG CTC TTT GTG CTG GTG GCT CCC AGC TGC  
170 180  
ala tyr gln val cys gly pro pro leu tyr gln leu gly ala ala  
GCC TAC CAG GTG TGC GGG CCG CCG CTG TAC CAG CTC GGC GCT GCC  
190  
thr gln ala arg pro pro pro his ala ser gly pro arg arg arg  
ACT CAG GCC CGG CCC CCG CCA CAC GCT AGT GGA CCC CGA AGG CGT

FIG. 74

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99/103

200 210  
leu gly cys glu arg ala trp asn his ser val arg glu ala gly  
CTG GGA TGC GAA CGG GCC TGG AAC CAT AGC GTC AGG GAG GCC GGG

220  
val pro leu gly leu pro ala pro gly ala arg arg arg gly gly  
GTC CCC CTG GGC CTG CCA GCC CCG GGT GCG AGG AGG CGC GGG GGC

230 240  
ser ala ser arg ser leu pro leu pro lys arg pro arg arg gly  
AGT GCC AGC CGA AGT CTG CCG TTG CCC AAG AGG CCC AGG CGT GGC

250  
ala ala pro glu pro glu arg thr pro val gly gln gly ser trp  
GCT GCC CCT GAG CCG GAG CGG ACG CCC GTT GGG CAG GGG TCC TGG

260 270  
ala his pro gly arg thr arg gly pro ser asp arg gly phe cys  
GCC CAC CCG GGC AGG ACG CGT GGA CCG AGT GAC CGT GGT TTC TGT

280  
val val ser pro ala arg pro ala glu glu ala thr ser leu glu  
GTG GTG TCA CCT GCC AGA CCC GCC GAA GAA GCC ACC TCT TTG GAG

290 300  
gly ala leu ser gly thr arg his ser his pro ser val gly arg  
GGT GCG CTC TCT GGC ACG CGC CAC TCC CAC CCA TCC GTG GGC CGC

310  
gln his his ala gly pro pro ser thr ser arg pro pro arg pro  
CAG CAC CAC GCG GGC CCC CCA TCC ACA TCG CGG CCA CCA CGT CCC

320 330  
trp asp thr pro cys pro pro val tyr ala glu thr lys his phe  
TGG GAC ACG CCT TGT CCC CCG GTG TAC GCC GAG ACC AAG CAC TTC

340  
leu tyr ser ser gly asp lys glu gln leu arg pro ser phe leu  
CTC TAC TCC TCA GGC GAC AAG GAG CAG CTG CGG CCC TCC TTC CTA

350 360  
leu ser ser leu arg pro ser leu thr gly ala arg arg leu val  
CTC AGC TCT CTG AGG CCC AGC CTG ACT GGC GCT CGG AGG CTC GTG

370  
glu thr ile phe leu gly ser arg pro trp met pro gly thr pro  
GAG ACC ATC TTT CTG GGT TCC AGG CCC TGG ATG CCA GGG ACT CCC

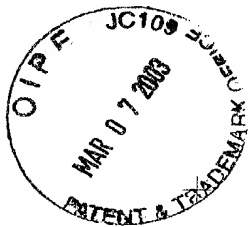
380 390  
arg arg leu pro arg leu pro gln arg tyr trp gln met arg pro  
CGC AGG TTG CCC CGC CTG CCC CAG CGC TAC TGG CAA ATG CGG CCC

400  
leu phe leu glu leu leu gly asn his ala gln cys pro tyr gly  
CTG TTT CTG GAG CTG CTT GGG AAC CAC GCG CAG TGC CCC TAC GGG

410 420  
val leu leu lys thr his cys pro leu arg ala ala val thr pro  
GTG CTC CTC AAG ACG CAC TGC CCG CTG CGA GCT GCG GTC ACC CCA

FIG. 74  
(CONTINUED)

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## 100/103

430  
ala ala gly val cys ala arg glu lys pro gln gly ser val ala  
GCA GCC GGT GTC TGT GCC CGG GAG AAG CCC CAG GGC TCT GTG GCG

440  
ala pro glu glu glu asp thr asp pro arg arg leu val gln leu  
GCC CCC GAG GAG GAG GAC ACA GAC CCC CGT CGC CTG GTG CAG CTG

460  
leu arg gln his ser ser pro trp gln val tyr gly phe val arg  
CTC CGC CAG CAC AGC AGC CCC TGG CAG GTG TAC GGC TTC GTG CCG

470  
ala cys leu arg arg leu val pro pro gly leu trp gly ser arg  
GCC TGC CTG CGC CGG CTG GTG CCC CCA GGC CTC TGG GGC TCC AGG

480  
his asn glu arg arg phe leu arg asn thr lys lys phe ile ser  
CAC AAC GAA CGC CGC TTC CTC AGG AAC ACC AAG AAG TTC ATC TCC

490  
leu gly lys his ala lys leu ser leu gln glu leu thr trp lys  
CTG GGG AAG CAT GCC AAG CTC TCG CTG CAG GAG CTG ACG TGG AAG

500  
met ser val arg asp cys ala trp leu arg arg ser pro gly val  
ATG AGC GTG CGG GAC TGC GCT TGG CTG CGC AGG AGC CCA GGG GTT

510  
gly cys val pro ala ala glu his arg leu arg glu glu ile leu  
GGC TGT GTT CCG GCC GCA GAG CAC CGT CTG CGT GAG GAG ATC CTG

520  
ala lys phe leu his trp leu met ser val tyr val val glu leu  
GCC AAG TTC CTG CAC TGG CTG ATG AGT GTG TAC GTC GTC GAG CTG

530  
leu arg ser phe phe tyr val thr glu thr thr phe gln lys asn  
CTC AGG TCT TTC TTT TAT GTC ACG GAG ACC ACG TTT CAA AAG AAC

540  
arg leu phe phe tyr arg pro ser val trp ser lys leu gln ser  
AGG CTC TTT TTC TAC CGG CCG AGT GTC TGG AGC AAG TTG CAA AGC

550  
ile gly ile arg gln his leu lys arg val gln leu arg glu leu  
ATT GGA ATC AGA CAG CAC TTG AAG AGG GTG CAG CTG CGG GAG CTG

560  
ser glu ala glu val arg gln his arg glu ala arg pro ala leu  
TCG GAA GCA GAG GTC AGG CAG CAT CGG GAA GCC AGG CCC GCC CTG

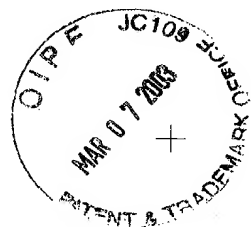
570  
leu thr ser arg leu arg phe ile pro lys pro asp gly leu arg  
CTG ACG TCC AGA CTC CGC TTC ATC CCC AAG CCT GAC GGG CTG CCG

580  
pro ile val asn met asp tyr val val gly ala arg thr phe arg  
CCG ATT GTG AAC ATG GAC TAC GTC GTG GGA GCC AGA ACG TTC CCG

FIG. 74  
(CONTINUED)

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## 101/103

650  
arg glu lys arg ala glu arg leu thr ser arg val lys ala leu  
AGA GAA AAG AGG GCC GAG CGT CTC ACC TCG AGG GTG AAG GCA CTG

660  
phe ser val leu asn tyr glu arg ala arg arg pro gly leu leu  
TTC AGC GTG CTC AAC TAC GAG CGG GCG CGG CGC CCC GGC CTC CTG

670  
gly ala ser val leu gly leu asp asp ile his arg ala trp arg  
GGC GCC TCT GTG CTG GGC CTG GAC GAT ATC CAC AGG GCC TGG CGC

680  
thr phe val leu arg val arg ala gln asp pro pro pro glu leu  
ACC TTC GTG CTG CGT GTG CGG GCC CAG GAC CCG CCG CCT GAG CTG

690  
tyr phe val lys val asp val thr gly ala tyr asp thr ile pro  
TAC TTT GTC AAG GTG GAT GTG ACG GGC GCG TAC GAC ACC ATC CCC

700  
gln asp arg leu thr glu val ile ala ser ile ile lys pro gln  
CAG GAC AGG CTC ACG GAG GTC ATC GCC AGC ATC ATC AAA CCC CAG

710  
asn thr tyr cys val arg arg tyr ala val val gln lys ala ala  
AAC ACG TAC TGC GTG CGT CGG TAT GCC GTG GTC CAG AAG GCC GCC

720  
his gly his val arg lys ala phe lys ser his val ser thr leu  
CAT GGG CAC GTC CGC AAG GCC TTC AAG AGC CAC GTC TCT ACC TTG

730  
thr asp leu gln pro tyr met arg gln phe val ala his leu gln  
ACA GAC CTC CAG CCG TAC ATG CGA CAG TTC GTG GCT CAC CTG CAG

740  
glu thr ser pro leu arg asp ala val val ile glu gln ser ser  
GAG ACC AGC CCG CTG AGG GAT GCC GTC GTC ATC GAG CAG AGC TCC

750  
ser leu asn glu ala ser ser gly leu phe asp val phe leu arg  
TCC CTG AAT GAG GCC AGC AGT GGC CTC TTC GAC GTC TTC CTA CGC

760  
phe met cys his his ala val arg ile arg gly lys ser tyr val  
TTC ATG TGC CAC CAC GCC GTG CGC ATC AGG GGC AAG TCC TAC GTC

770  
gln cys gln gly ile pro gln gly ser ile leu ser thr leu leu  
CAG TGC CAG GGG ATC CCG CAG GGC TCC ATC CTC TCC ACG CTG CTC

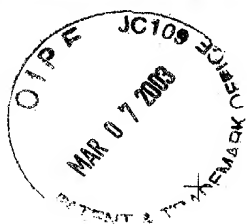
780  
cys ser leu cys tyr gly asp met glu asn lys leu phe ala gly  
TGC AGC CTG TGC TAC GGC GAC ATG GAG AAC AAG CTG TTT GCG GGG

790  
ile arg arg asp gly leu leu leu arg leu val asp asp phe leu  
ATT CGG CGG GAC GGG CTG CTC CTG CGT TTG GTG GAT GAT TTC TTG

800  
810  
820  
830  
840  
850  
860  
870

FIG. 74  
(CONTINUED)

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## 102/103

880  
leu val thr pro his leu thr his ala lys thr phe leu arg thr  
TTG GTG ACA CCT CAC CTC ACC CAC GCG AAA ACC TTC CTC AGG ACC

890  
leu val arg gly val pro glu tyr gly cys val val asn leu arg  
CTG GTC CGA GGT GTC CCT GAG TAT GGC TGC GTG GTG AAC TTG CGG

910  
lys thr val val asn phe pro val glu asp glu ala leu gly gly  
AAG ACA GTG GTG AAC TTC CCT GTA GAA GAC GAG GCC CTG GGT GGC

920  
thr ala phe val gln met pro ala his gly leu phe pro trp cys  
ACG GCT TTT GTT CAG ATG CCG GCC CAC GGC CTA TTC CCC TGG TGC

940  
gly leu leu leu asp thr arg thr leu glu val gln ser asp tyr  
GGC CTG CTG CTG GAT ACC CGG ACC CTG GAG GTG CAG AGC GAC TAC

950  
ser ser tyr ala arg thr ser ile arg ala ser val thr phe asn  
TCC AGC TAT GCC CGG ACC TCC ATC AGA GCC AGT GTC ACC TTC AAC

960  
arg gly phe lys ala gly arg asn met arg arg lys leu phe gly  
CGC GGC TTC AAG GCT GGG AGG AAC ATG CGT CGC AAA CTC TTT GGG

970  
val leu arg leu lys cys his ser leu phe leu asp leu gln val  
GTC TTG CGG CTG AAG TGT CAC AGC CTG TTT CTG GAT TTG CAG GTG

980  
asn ser leu gln thr val cys thr asn ile tyr lys ile leu leu  
AAC AGC CTC CAG ACG GTG TGC ACC AAC ATC TAC AAG ATC CTC CTG

1000  
leu gln ala tyr arg phe his ala cys val leu gln leu pro phe  
CTG CAG GCG TAC AGG TTT CAC GCA TGT GTG CTG CAG CTC CCA TTT

1010  
his gln gln val trp lys asn pro thr phe phe leu arg val ile  
CAT CAG CAA GTT TGG AAG AAC CCC ACA TTT TTC CTG CGC GTC ATC

1020  
ser asp thr ala ser leu cys tyr ser ile leu lys ala lys asn  
TCT GAC ACG GCC TCC CTC TGC TAC TCC ATC CTG AAA GCC AAG AAC

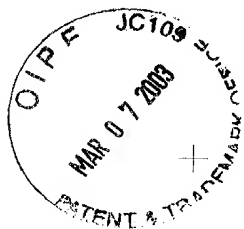
1030  
ala gly met ser leu gly ala lys gly ala ala gly pro leu pro  
GCA GGG ATG TCG CTG GGG GCC AAG GGC GCC GCC GGC CCT CTG CCC

1040  
ser glu ala val gln trp leu cys his gln ala phe leu leu lys  
TCC GAG GCC GTG CAG TGG CTG TGC CAC CAA GCA TTC CTG CTC AAG

1050  
leu thr arg his arg val thr tyr val pro leu leu gly ser leu  
CTG ACT CGA CAC CGT GTC ACC TAC GTG CCA CTC CTG GGG TCA CTC

FIG. 74  
(CONTINUED)

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103/103

1100 1110  
arg thr ala gln thr gln leu ser arg lys leu pro gly thr thr  
AGG ACA GCC CAG ACG CAG CTG AGT CGG AAG CTC CCG GGG ACG ACG

1120  
leu thr ala leu glu ala ala ala asn pro ala leu pro ser asp  
CTG ACT GCC CTG GAG GCC GCA GCC AAC CCG GCA CTG CCC TCA GAC

1130 1132  
phe lys thr ile leu asp OP  
TTC AAG ACC ATC CTG GAC TGA TGGCCACCCGCCACAGCCAGGCCGAGAGCAGA

CACCAGCAGCCCTGTCACGCCGGGCTCTACGTCCCAGGGAGGGAGGGGCGGCCACACCC  
AGGCCCGCACCGCTGGGAGTCTGAGGCCTGAGTGAGTGTTTGGCCGAGGCCTGCATGTCC  
GGCTGAAGGCTGAGTGTCGGGCTGAGGCCTGAGCGAGTGTCAGCCAAGGGCTGAGTGTC  
CAGCACACCTGCCGTCTTCACTTCCCCACAGGCTGGCGCTCGGCTCCACCCAGGGCCAG  
CTTTTCYTCACCAGGAGCCCGGCTTCCACTCCCCACATAGGAATAGTCCATCCCCAGATT  
CGCCATTGTTACCCYTCGCCCTGCCYTCCTTTGCCTTCCACCCCCACCATCCAGGTGGA  
GACCCTGAGAAGGACCCTGGGAGCTCTGGGAATTTGGAGTGACCAAAGGTGTGCCCTGTA  
CACAGGCGAGGACCCTGCACCTGGATGGGGGTCCCTGTGGGTCAAATTGGGGGGAGGTGC  
TGTGGGAGTAAATACTGAATATATGAGTTTTTCAGTTTTTGRAAAAAAAAAAAAAAAAAA  
AAAAAAAAA

FIG. 74  
(CONTINUED)

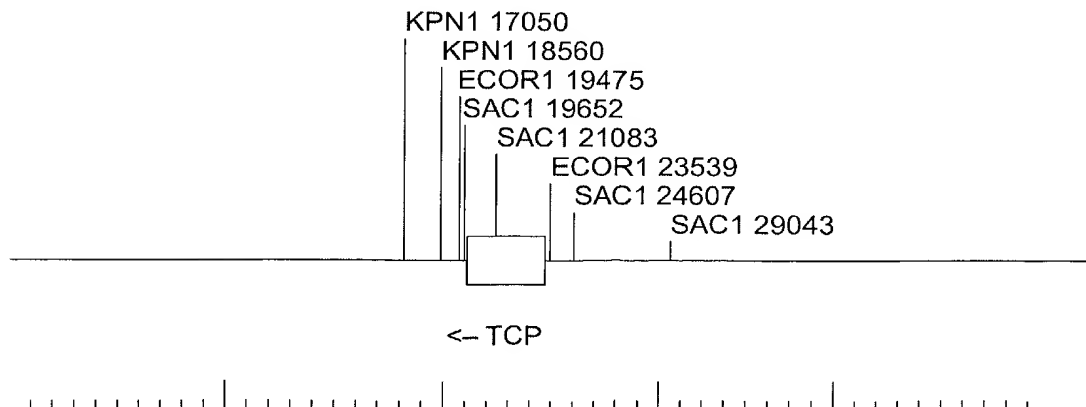


FIG. 75